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AR042946 Sequence			8121	G			-	_			_			-		O	Sequence	AR174747 Sequence		Seq		1626			CQ547633 Sequence

ALIGNMENTS

## 13; Unclassified. 1 (bases 1 to 54) Kunsch, C.A., Choi, G.A., AR538044 Sequence 2606 from patent AR538044 AR538044.1 GI:53929261 4 TTGCCACTCCCAT 16 Staphylococcus aureus polynucleotides and sequences Patent: US 6593114-A 2606 15-JUL-2003; Location/Qualifiers 1 (bases 1 to 54) Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A. AR356488 Sequence 2606 from patent AR356488 Unknown Unknown. Unknown. Unclassified. Unknown. AR356488.1 GI:33762572 Similarity TTGCCACTCCCAT 35 Conservative /organism="unknown" /mol\_type="genomic DNA" 65.0%; Score 13; 100.0%; Pred. No. cive 0; Mismatch Mismatches 54 US 54 US bp DNA 6593114. bp DNA 6737248. DB 6; Lo 0, Length 54; Indels linear linear PAT 17-AUG-2003 PAT 08-OCT-2004 0, Gaps 0

Barash, S.C., Dillon, P.J.,

Fannon, M.R. and

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                                                       Method of designing addressable array for detection of sequence differences using ligase detection reaction patent: WO 0179548-A 5395 25-0CT-2001; CORNELL RESEARCH FOUNDATION, INC. (US)
                                                                                                                                          synthetic construct synthetic construct other sequences; artificial sequences.
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Sequence 5395 from Patent
AX293633
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Staphylococcus aureus polynucleotides and sequences
Patent: US 6737249-A 2606 18-MAY-2004,
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               /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
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/mol_type="unassigned DNA"
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1 (bases 1 to 21)

1 (bases 1 to 21)

Ballinger, D.G., Ding, W., Wagner, S. and Hess, M.A. Chromosome 11-linked coronary heart disease susce
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Hypothetical Probe Sequence"
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G-protein coupled receptors and nucleic acids encoding same Patent: WO 02059313-A 502 01-AUG-2002;
Curagen Corporation (US)
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AX703273
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/db_xref="taxon:32630"
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/mal_type="unassigned DNA"
/mal_type="taxon:32630"
/note="PCR Primer Sequence"
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AR065274/c
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AR039144/c
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Amaral, M.Catherine. and Chen, J.-L.
Regulators of UCP2 gene expression
Patent: US 5807740-A 8 15-SEP-1998;
Location/Qualifiers
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Sequence 8 from patent US
AR065274
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         other sequences; artificial sequences.

1 (bases 1 to 29)

Amaral, C.M. and Chen, J.L.

Regulators of UCP2 gene expression

Patent: JP 2001507943-A 8 19-JUN-2001;
                                                                             synthetic construct synthetic construct
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BD061658
BD061658.1 GI:22607263
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Amaral, M. Catherine. and Chen, J.-L.
Method of identifying agents that modulate
Patent: US 5849514-A 8 15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
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/mol_type="unassigned DNA"
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                Picoult-Newburg,L. and Pohl,M.
Genotyping reagents, kits and methods of use thereof
Patent: WO 0129362-A 1336 26-APR-2001;
Orchid BioSciences, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                         27
                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Sequence 1336 from Patent
AX116213
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27 CACTCCCATTCT 16
                                                                                                             Homo sapiens (human)
Homo sapiens
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Sequence 8 1
AR128133
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Location/Qualifiers
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PD 19-JUN-2001
PF 22-APR-1998 JP 1998547120
PF 25-APR-1997 US 08/846012
PI CATHERINE M AMARAL, JIN LONG CHEN
PC C12N1/00, C12N5/10, C12N15/11, C12N15/63, C12Q1/02, C12Q1/68
Strandedness: Double;
CC Topology: Linear;
PH Key Location/Qualifiers.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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6183956.
                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        DB 6; Lo
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1.4e+04;
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AX159372/c
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                                                        FEATURES
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AX159371/c
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                                                                                                                                           Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa;
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                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide
methods of use thereof
Patent: WO 0140521-A 2700 07-JUN-2001;
Curagen Corporation (US)
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Sequence 2700 from Patent
AX159372
AX159372.1 GI:14540703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methods of use thereof
Patent: WO 0140521-A 2699 07-JUN-2001;
Curagen Corporation (US)
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Sequence 2699 from Patent
AX159371
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
                                                                   Location/Qualifiers
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Accession number cg42330545"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 1.4e+04;
tive 0; Mismatches 0;
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Pred. No. 1.4e+04;
0; Mismatches 0;
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Catarrhini; Hominidae;
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AX159373/c
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AX165283/c
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              variation
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AX159373
AX159373.1 GI:14540704
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Nucleic acids containing single nucleotide polymorphisms
methods of use thereof
Patent: WO 0140521-A 2701 07-JUN-2001;
Curagen Corporation (US)
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AX165283
AX165283.1 GI:14546112
                                                                                            Nucleic acids containing single nucleotide polymorphisms and methods of use thereof Patent: WO 0138586-A 478 31-MAY-2001; Curagen Corporation (US)
                                                                                                                                                 Shimkets, R.A. and Leach, M.
                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Accession number cg42330545"
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/note="single nucleotide polymorphism
                                                                              ocation/Qualifiers
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100.0%; Pred. No. 1.4e+04;
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WO0138586.
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HUMUT5280A
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CQ545434/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Rel
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: CACTCCAGCCTGGGCAATAAGAG
Primer B: GGTAGCTCTGTTGCACATGACAAGT
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
Sequence 15069 from Patent CQ545434 CQ545434.1 GI:41511698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 55)
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STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; mononucleotide repeat; sequence tagged site.
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Human STS UT5280, 5' primer bind, sequence
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.4e+04;
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                                    60 bp DNA WO0210449.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 66)
Sironi,M., Pozzoli,U., Cagliani,R., Giorda,R., Comi,G.P., Bardoni,A., Menozzi,G. and Bresolin,N.
                                                                                                                          AY139609
Homo sapiens dystrophin
AY139609
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Sequence 17268 from Patent
CQ547633
CQ547633.1 GI:41513897
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Mammalia; Eutheria;
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.4e+04;
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Sequence 5 from patent US
AR241626
AR241626.1 GI:27287383
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AR040149
AR040149.1 GI:5959512
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                                                                                                             CATTGCCACTC 16
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Bardoni, A., Menozzi, G.
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1 (bases 1 to 17)
Stinchcomb,D.T. and McSwiggen,J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 997 15-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-AUG-2002) I.R.C.C.S. E.Medea, Ass. La Nostra Famiglia, Via Don L. Monza, 20, Bosisio Parini, LC 23842, Italy Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Relevance of sequence and structure elements the dystrophin gene major hot-spot Unpublished 2 (bases 1 to 66)
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997 from patent US 5807743.
                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned DNA"
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36. .>66
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|mol_type="genomic DNA"
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Pred. No.
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18 bp
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AR258715
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Biering, E. and Krossoy, B.
Biering, E. and Krossoy, B.
DNA encoding structural protein-1 of
virus and uses thereof
Patent: US 6471964-A 5 29-OCT-2002;
Location/Qualifiers
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Roy,A.K. and Chen,S.
Ribozyme mediated inactivation of the androgen receptor
Patent: US 6489163-A 5 03-DEC-2002;
Location/Qualifiers
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                                             Patent: EP 1094069-A 5 25-APR-2001;
Akzo Nobel N.V. (NL)
                                                                        Biering,E. and Krossoy,B.

Dna encoding structural protein-1 of infectious virus and uses thereof
                                                                                                                        Infectious salmon anemia virus Infectious salmon anemia virus Viruses; seRNA negative-strand unclassified Orthomyxoviridae.
                                                                                                                                                                                      AX137953.1 GI:14274051
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
organism="Infectious salmon anemia virus"
|mol_type="unassigned DNA"
                                    Location/Qualifiers
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100.0%; Pr
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6e+04;
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                                                                                                                                      Orthomyxoviridae;
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                                                                                      salmon anaemia
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BD015843/c
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AR174747
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: JP 2001211888-A 2 07-AUG-2001;
AKZO NOBEL NV
OS Infectiuos salmon anaemia virus
PN JP 2001211888-A/2
PD 07-AUG-2001
PF 17-CCT-2000 JP 2000316583
PF 17-CCT-2000 JP 2000316583
PF 18-CCT-1999 EP 99203401.7
PI BILLING A ERIC, KLOSSEI B BEYORN
PC C12015/09,A61K38/00,A61K39/145,A61P2
PC C12015/09,A61K38/00,A61K39/145,A61P2
PC C12015/68
PC G01N33/569//C12P21/08,C12N15/00,A61P2
PC G01N33/569/C12P21/08,C12N15/00,A61P2
PC G01N33/569/C12P21/08,C12N15/00,A61P2
PC G01N33/569/C12P21/08,C12N15/00,A61P2
PC G01N31/569/C12P21/08,C12N15/00,A61P2
PC G10N31/569/C12P21/08,C12N15/00,A61P2
PC G10N31/569/C12P21/08,C
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DNA encoding structure protein-1 and utilization thereof.
BD015843

BD015843.1 GI:22556980
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Sequence
AR174747
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Eric,B.A. and Beyorn,K.B.
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1 (bases 1 to 19)
Rauscher,F.J. III and Jensen,D.E.
BRCAl associated polynucleotide (BAP-1) and uses therefor
                                                                                                  Unknown
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                                                                                                                         Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infectious salmon anaemia virus
JP 2001211888-A/2
O7-AUG-2001
17-OCT-2000 JP 2000316583
18-OCT-1999 EP 99203401.7
BILLING A ERIC, KLOSSEI B BEYORN
C12N15/09, A61K38/00, A61K39/145, A61P31/12, C07K14/11, C07K16/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C12Q1/68,
G01N33/569//C12P21/08,C12N15/00,A61K37/02
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1. .18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                                                                                                                                                       GI:17915067
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6e+04;
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E infectious salmon anemia
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PAT 17-JUL-2003

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KEYWORDS
SOURCE
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A83708/c
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ACCESSION
         Query Match 55.0%; Score 11; DB 6; L
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0;
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                                                                                                                      APOPTIC CELL DEATH PATHWAYS

APOPTIC CELL DEATH PATHWAYS

Patent: WO 9849291-A 4 05-NOV-1998;

RICCARDI CARLO (IT); APPLIED RESEARCH SYSTEMS

LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                     1 (bases 1 to 20)
Riccardi,C.
INTRACELLULAR GLUCOCORTICOID-INDUCED LEUCINE ZIPPERS MODULATORS OF
                                                                                                                                                                                                                                                   unidentified
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                                                                                                                                                                                                                           unclassified
                                                                                                                                                                                                                                                                               A83708.1
                                                                                                                                                                                                                                                                                             Sequence 4 from Patent WO9849291.
                                                                                                                                                                                                                                                                                                                    A83708
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Intracellular modulators of apoptopic cell death pathways
Patent: EP 0884385-A 4 16-DEC-1998;
APPLIED RESEARCH SYSTEMS (AN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 bp
Sequence 4 from Patent Ep0884385,
A82791
A82791.1 GI:6732470
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11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%; So ilarity 100.0%; I Conservative 0;
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                                                                           /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                            GI:6732944
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Location/Qualifiers
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/mol_type="unassigned DNA"
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100.0%; Pr
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Pred. No. 5.9e+04;
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Pred. No.
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6e+04;
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SOURCE
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ACCESSION
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CQ757498/c
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VERSION
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BD274392
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Human vanilloid receptor and use thereof
Patent: JP 2002531085-A 29 24-SEP-2002;
GLAXO GROUP LITD
OS Artificial Sequence
PN JP 2002531085-A/29
PD 24-SEP-2002
PP 30-NOV-1999 JP 2000585397
PF 30-NOV-1999 GB 9826359.3
PI NATALIE SAMANTHA DELANY,PHILIPPE SANSE
PC C12N15/09,A61K45/00,A61P1/00,A61P11/00
                                                                                                                                                                                                 CQ757498
Sequence 9
CQ757498
                              Method for predicting a drug transport capability by abcg2 polymorphisms
Patent: WO 2003107249-A 9 24-DEC-2003;
BANYU PHARMACEUTICAL CO., LTD. (JP)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                             10 CTCCCATTCTT 20
                                                                                                                                            synthetic construct synthetic construct
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                                                                                                      Kotani, H. and Mizuarai, S.
                                                                                                                             other sequences; artificial sequences.
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JP 2002531085-A/29.
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                                                                                                                                                                                                                                                                                                                                           Conservative
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C12N5/10, C12P21/02, C12Q1/02// (C12P21/02, C12R1:91), C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A61P25/04, A61P25/06, A61P25/28, A61P29/00, A61P29/00, C07K14/705,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-1999 JP 2000585397
01-DEC-1998 GB 9826359.3
NATALIE SAMANTHA DELANY, PHILIPPE SANSEAU, SIMON NICHOLAS TATE
C12N15/09, A61K45/00, A61P1/00, A61P11/00, A61P11/06, A61P13/00, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence: Primer 
Location/Qualifiers
organism="synthetic construct"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Artificial
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                           from Patent WO2003107249.
                                                                                                                                                                                    GI:44847536
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PAT 01-MAR-2004

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RESULT 33
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AX026882
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source
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                     Intracellular modulator in apoptosis cell death pathway

Patent: JP 2001523102-A 3 20-NOV-2001;
APPLIED RESEARCH SYSTEMS ARS HOLDING NV
OS Mus sp. (mouse)
PN JP 2001523102-A/3
PD 20-NOV-2001
PF 27-APR-1998 JP 1998546599
PF 27-APR-1997 EP 97107033.9
PC C12N15/12,C07K14/47,G01N33/50,A61K38/17,A61K48/00,C12N
PCR reverse primer
FH Key Location/Qualifiers.
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BD082732
BD082732.1 GI:22628342
JP 2001523102-A/3.
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Human vanilloid receptors and their uses
Patent: WO 0032766-A 35 08-JUN-2000;
DELANY NATALIE SAMANTHA (GB); TATE SIMON
GROUP LTD (GB); SANSEAU PHILIPPE (GB)
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Sequence 35 from Patent WO0032766.
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                                                 CARLO RICCARDI C12N15/12, C07K14/47, G01N33/50, A61K38/17, A61K48/00, C12N5/10 CC
Location/Qualifiers
1. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol type="unassigned DNA"
/db xref="texon:32630"
/noTe="primer"
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/note="Exon 4 forward|
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Pred. No.
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CQ831007
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Sequence
CQ831007
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Beta-catenin oligonucleotide michrochip and method for detecting beta-catenin mutations employing same patent: Ep 1437417-A 92 14-JUL-2004;

National Cancer Center (KR)

Location/Qualifiers
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                                                                                                                                                                        Good, X.C. and Monis, J.
Grapevine leafroll-associated virus proteins
Patent: WO 0105957-A 29 25-JAN-2001;
                                                                                                                                                                                                                                                synthetic construct synthetic construct
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AX077873
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55.0%; Score 11; DB 6; Lilarity 100.0%; Pred. No. 5.9e+04; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                      /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="ttaxon:32630"
/noTe="primer"
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Pred. No. 5.9e+04;
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BD102253
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Sequence
AX166683
                                        Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clary,D.S.

Novel human protein kinases and protein kinase-like enzymes

Patent: WO 0138503-A 174 31-MAY-2001;

Sugen, Inc. (US)
                                                                                                                                  synthetic construct synthetic construct
                                                                                                                   other sequences; artificial sequences
                                                                                                                                                                   AX166683.1 GI:14546958
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1 (bases 1 to 22)
Nagano, M., Ito, M., Sagehashi, Y., Hattori, H., Egashira, T., Yamashita, S. and Matsuzawa, Y.
Method of detecting risk factor for onset of arteriosclerosis Patent: WO 0.171032-A 16 27-SEP-2001;
BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI, TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
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WO 0171032-A/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
23-MAR-2001 WO 2001JP002327
24-MAR-2000 JP 00P 084264
MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI, TORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method
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WO 0171032-A/16
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organism="synthetic construct"
/mol_type="unassigned DNA"
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Secreted proteins and pol
BD140471
BD140471.1 GI:23235416
JP 2002506611-A/21.
Bynthetic construct
Synthetic construct
  Secreted proteins and polynucleotides encoding them Patent: JP 2002506611-A 21 05-MAR-2002; GENETICS INSTITUTE INC OS Artificial Sequence PN JP 2002506611-A/21 PD 05-MAR-2002 PF 24-NOV-1998 JP 2000522118 PD 05-MAR-2002 PF 24-NOV-1998 JP 2000522118 FR 26-NOV-1997 US 60/066804,23-NOV-1998 US KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA J
                                                                                                                                                                           other sequences; artificial sequences.

1 (bases 1 to 29)

Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A.C., Evans, C., Merberg, D., Treacy, M., Agostino, M.J., Ii, R.J.S., Wong, G.G., Clark, H.F. and Fechtel, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max (soybean)
Glycine max
Glycine max
Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Patent: WO 0151627-A 528 19-JUL-2001;
MONSANTO COMPANY (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:3847"
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/note="Primer"
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El (bases 1 to 29)

El (bases 1 to 29)

Is Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,

Treacy,M., Spaulding,V. and Agostino,M.J.

Secreted proteins and polynucleotides encoding them

Patent: JP 2002510196-A 12 02-APR-2002;

PR 19 2002510196-A/12

PD 02-APR-1998 JP 1998544380

PR 15-APR-1997 US 08/843374,13-APR-1998 US 09/059487 PI

KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI

DAVID MERBERG,

PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC

C12N15/12,C07K14/47,A61K38/17

CC Jdesc='Oligonucleotide'

FH Key Location/Qualifiers

Is castion/Qualifiers
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BD191485 .

BD191485 .1 GI:33001224

JP 2002510196-A/12.

unidentified
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PC A61P29/00,A61P35/00,A61P37/04,A61P37/06,C12N15/00,C12N5/00 CC oligonuclectide CC biotinylated phosphoaramidite residue FH Key Location/Qualifiers FT misc_feature (2).
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                                                                                                                                                   Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 1 from Patent WO02062943.
AX512846
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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5.8e+04;
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AR042946/c
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                                              l (bases 1 to 42)
Lonberg, N. and Kay, R.M.
Transgenic non-human animals for producing
Patent: US 5814318-A 32 29-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 42)

1 (bases 1 to 42)

1 conberg,N. and Kay,R.M.

Transgenic non-human animals for producing Transgenic non-human avaimals for producing Datent: US 5789650-A 32 04-AUG-1998;

Location/Qualifiers
                                                                                                                               Unknown.
                                                                                                                                                                    AR042946 42 bp
Sequence 32 from patent US 5814318.
AR042946 GI:5963954
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                                                                                                                                               Unknown.
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AR021384
AR021384.1 GI:3975999
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Use of oligonucleotides for improving plasmid transfection cells, transfection method and kit
Patent: WO 02062943-A 1 15-AUG-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR); I
GUSTAVE ROUSSY (FR)
                                                                                                                   Unclassified.
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                        organism="unknown"
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/mol_type="unassigned DNA"
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Search completed: September 14, 2005, 11:03:30 Job time: 2625 secs

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Minimum DB
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Aai75760 Human sil	Aal55696 Human zin	Aaz28769 G-less ol	Aav08886 PCR prime	Aav44981 PCR prime	Adi04496 Human G-p	Abq88545 Human GPC	Abs59154 Human G-p	Abi83920 Capture o	Abi83921 Capture o	Ads31699 Gene expr	Aaz26938 Human chr	Adn31527 Human for	Adn31409 Human for	Adn31408 Human for	Abi93675 Capture o	Abh67956 Oligonucl	Abh69241 Oligonucl	Abn45267 Human spl	Aav76917 Staphyloc	Description

## ALIGNMENTS

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RESULT 1
AAV76917/c
Staphylococcus aureus contig SEQ ID #2606.
                                                                                                                        AAV76917;
                                                                                                                              AAV76917 standard; DNA; 54 BP.
                                                                                           toxic shock syndrome; ds.
                                                                                                                 16-MAR-1999
                                                                                                                  (first entry)
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Computer readable medium; vaccine; S.aureus infection; immunodetection cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; Staphylococcus aureus immunodetection;

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-00100117

05-JAN-1996; 96US-0009861P

(HUMA-) HUMAN GENOME SCI INC

Kunsch CA, Choi GH, Barash SC, Dillon Pq, Fannon ₹, Rosen Ç,

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived stored on computer readable medium and S.aureus vaccines. from Staphylococcus aureus - in the production of anti-

Claim 1; Page 2287; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or 얹

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RESULT 2
ABN45267
ID ABN4
XX ABN4
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (gub-transcriptome comprises messenger RNAs transcribed from multiple coligonucleotides, each capable of hybridising selectively to a set of which encodes one or more messenger RNAs transcription unit of the genome, oligonucleotide ilbraries are useful for detecting mixing trom a gloven transcription unit of the genome, oligonucleotide libraries are useful for detecting mixing from a gloven transcription of the genome, oligonucleotide libraries are useful for detecting mixing from a quantitatively characterising the corresponding transcriptome, and in quantitatively characterising the corresponding transcriptome, and in transcriptomes. The libraries may also be used as specialised mini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 18015; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000;
02-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUL-2001; 2001WO-IB001903.
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Best Local
       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The range of diseases are used for diagnosis and/or prognosis of cancer and a central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH32073 data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                       Claim 1; SEQ ID NO 269218; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                       WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory, immune, motalication
                                                                                                                                                                                                                                                                                                                                                                (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                      07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-IB000713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a pattent suffering from a particular rate, humans and mice, which are used in the exemplification of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200177384-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 269218 for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABH69241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABH69241 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60
                                                                                                                                                                                                                                                                                                                                                             EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TTGCCACTCCCAT 16
                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCCACTCCCAT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 12 A; 14 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system; gastrointestinal; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.0%; Su
100.0%; Pr
                                                                                                                                                                                                                                                                                                                              Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                              ζ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP TSC0001665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune;
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Sequence 12

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                                                                                                                                    Matches
                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 267933 for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                               Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS AG.
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 267933; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                      CCACTCCCATTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                    Conservative
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                                                                                                                                                   60.0%; Score 12; DB 5; L
100.0%; Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin
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                                                                                                                                    0
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Pred. No.
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                                                                                                                                      Mismatches
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                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP TSC0000710.
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ABI93675 standard; DNA; 20 BP

RESULT 6
ADN31408
ID ADN3

ADN31408 standard; DNA; 20

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Matches 12
                                                                                                                                                                                                                                                                                                                           Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, p33 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. ABH2074 to ABH207546 represent oligonucleotide sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (MI) for designing capture oligonuclectide probes (II) will hybridise with little mismatch, where oligonuclectide probes (II) will hybridise with little mismatch, where (I) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal infectious agents e.g. Cryptococcus neoformans, Candida albicans and Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus, Epstein-Barr virus and polio virus, and parasitic infectious agents selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus medinesis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; K-ras; PCR primer; probe; capture probe; mutation detection; ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Designing capture oligonucleotide probes complementary oligonucleotides hybridize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barany F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2001; 2001WO-US010958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capture oligonucleptide Zip ID#762 oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 29; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-2000; 2000US-0197271P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABI93675;
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC
15
                                                     1 GCATTGCCACTC 12
                                                                                                                                l Similarity
                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                                                                                                                        B₽;
                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                     5 A; 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerry NP,
                                                                                                                                                                 60.0%; Score 12; DB 6; 1
100.0%; Pred. No. 3.3e+03
                                                                                                                                                                                                                                                                        8 G; 3 T; 0 U; 0 Other;
                                                                                                                                    0;
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Favis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for use on a support to which with little mismatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kliman
                                                                                                                                                                                                    Length
                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                              The invention relates to a new compound 8-80 nucleobases in length (an antisense oligonucleotide) targeted to a nucleic acid molecule encoding forkhead box C2, where the compound specifically hybridises with the nucleic acid molecule encoding human forkhead box C2 appearing as ADN31339 and inhibits the expression of forkhead box C2 in cells or tissues, screening for a modulator of forkhead box C2 in cells or tissues, screening for a modulator of forkhead box C2, a diagnostic method for identifying a disease state, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with forkhead box C2. The compound and methods are useful in diagnosing and treating developmental disorders e.g. lympoedemas such as lympoedema-distichiasis, dysgeneses of the mouse irridocorneal angle similar to those seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The present sequence is an antisense oligonucleotide targeting forkhead box
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compound targeted to a nucleic acid molecule encoding forkhead C2, useful in diagnosing and treating developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 15; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-399740/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2002; 2002US-00303635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-2002; 2002US-00303635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lympoedema; lymp
Axenfeld-Rieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN31408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      forkhead box C2 antisense oligonucleotide ISIS227188
                                                                                                                                 Similarity
GCATTGCCACTC 17
                                                     GCATTGCCACTC 12
                                                                                                                                                                                                                  20
                                                                                                          Conservative
                                                                                                                                                                                                          BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/mod_base= OTHER
/note= "2'-methoxyethyl residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anomaly; congenital glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorothioate backbone and methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mod base= OTHER
                                                                                                                           60.0%; Score 12; DB 12; 100.0%; Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _base≃ OTHER
e= "2'-methoxyethyl residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; 80pp; English.
                                                                                                     ;
                                                                                                        Mismatches
                                                                                                     0;
                                                                                                                                                     Length 20
                                                                                                     Indels
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                                                                                                     0
                                                                                               Gaps
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Query Match Best Local Similarity

60.0%; Score 12; DB 12; 100.0%; Pred. No. 3.3e+03;

Length 20; Indels

0,

Gaps

0

20

BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0

Other;

Matches

12;

Conservative

0

Mismatches

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RESULT 7
ADM31409
ID ADM3
XX ADM3
AC A
                                                                             The invention relates to a new compound 8-80 nucleobases in length (an antisense oligonucleotide) targeted to a nucleic acid molecule encoding forkhead box C2, where the compound specifically hybridises with the nucleic acid molecule encoding human forkhead box C2 appearing as ANN31339 and inhibits the expression of forkhead box C2 appearing as screening for a modulator of forkhead box C2 in cells or tissues, screening for a modulator of forkhead box C2, a diagnostic method for identifying a disease state, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with forkhead box C2. The compound and methods are useful in diagnosing and treating developmental disorders e.g. lympoedemas such as lympoedema-distichiasis, dysgeneses of the mouse irridocorneal angle similar to those seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The present sequence is an antisense oligonucleotide targeting forkhead box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; SEQ ID NO 74; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compound targeted to a nucleic acid molecule encoding forkhead C2, useful in diagnosing and treating developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-399740/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2002; 2002US-00303635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2002; 2002US-00303635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss; antisense; forkhead box C2; developmental disorder. lympoedema; lympoedema-distichiasis; dysgenesis; iridocorneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human forkhead box C2 antisense oligonucleotide ISIS227189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN31409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lympoedema-distichiasis; dysgenesis; iridocorneal angle; ger anomaly; congenital glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "
16. .20
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/mod_ba
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/note= "Phosphorothioate backbone and all cytidines
-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mod_base= OTHER
note= "2'-methoxyethyl residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _base= OTHER
e= "2'-methoxyethyl residue"
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RESULT 8
ADN31527/c
RESULT 9
AAZ26938
ID AAZ2
XX
AC AAZ2
XX
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                                                                                                                      맑
                                                                                                                                                 र्
                                                                                                                                                                                             Query Match
Best Local &
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                   The invention relates to a new compound 8-80 nucleobases in length (an antisense oligonucleotide) targeted to a nucleic acid molecule encoding forkhead box C2, where the compound specifically hybridises with the nucleic acid molecule encoding human forkhead box C2 appearing as ANN31339 and inhibits the expression of forkhead box C2 also included are inhibiting the expression of forkhead box C2 in cells or tissues, screening for a modulator of forkhead box C2, a diagnostic method for identifying a disease state, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with forkhead box C2. The compound and methods are useful in diagnosing and treating developmental disorders e.g. lympoedemas such as lympoedemadistichiasis, dysgeneses of the mouse irridocorneal angle similar to those seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The present sequence is a forkhead box C2 nucleic acid region targeted by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; antisense; forkhead box C2; developmental disorder; lympoedema; lympoedema-distichiasis; dysgenesis; iridocorneal angle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN31527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN31527 standard; cDNA;
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                        present sequence is a forkhead box antisense oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 16; SEQ ID NO 192; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compound targeted to C2, useful in diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-399740/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2002; 2002US-00303635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-2002; 2002US-00303635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Axenfeld-Rieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human forkhead box C2 cDNA AS target region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-2004
               AAZ26938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS
                                             AAZ26938 standard; DNA; 21 BP
                                                                                                                                                                             Local Similarity
hes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATTGCCACTC
                                                                                                                                                    GCATTGCCACTC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCATTGCCACTC 20
                                                                                                                                                                                                                                           20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anomaly; congenital glaucoma.
                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a nucleic acid molecule encoding forkhead box and treating developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                  0
                                                                                                                                                                                               Score 12;
Pred. No.
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                               DB 12; I
. 3.3e+03;
                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                    Indels
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BXAXAXI
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                                                                                                                        ADS31699
                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes the human chromosome 11-linked coronary compared to the germline are indicative of a predisposition to coronary heart disease or to metabolic disorders related to lipid metaboliam. Products from the CC present invention can be used in the diagnosis of predisposition to coronary heart disease and to metabolic disorders, including coronary heart disease and to metabolic disorders, including chypoalphalipoproteinaemia, familial combined hyperlipidaemia, insulin coronary heart disease and metabolic disorders, obesity, diabetes and dyslipidaemic hypertension. CHD1 proteins can be used for treating coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be coronary heart disease and metabolic disorders. The products can also be cared for detection and drug screening. ANZ26812 to ANZ27027 to ANZ27027 prepresent human CHD1 nucleotide sequences used in the cared in the identification of human CHD1; ANZ26842 to ANZ27014 represent pCR primers used in the screening of mutations in human CHD1; anzersent pCR primers used in the screening of mutations in human CHD1; anzersent invention.
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 11; diagnosis; screening; PCR primer; metabolic disorder; detection; hypoalphalipoproteinaemia; familial combined hyperlipidaemia; insulin resistant syndrome X; multiple metabolic disorder; obesity;
                                                                                                                                                                                                                                                                                                                                        Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated coronary heart disease susceptibility gene, used to develop products for diagnosis and treatment of coronary heart disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1998;
06-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes; dyslipidaemic hypertension; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; coronary heart disease susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 98; 297pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-540844/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ballinger DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1999.
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                                                                     ADS31699;
                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                         ADS31699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 11 linked
                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                   TTGCCACTCCCA 15
                                                                                                         standard;
                                                                                                                                                                                                  TTGCCACTCCCA
                                                                                                                                                                                                                                                                                                                                            BP; 6 A; 9 C; 2 G; 4 T; 0 U; 0
                                                                                                                                                                                                                                                                        Conservative
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98US-0080934P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US004682
                                                                                                         DNA;
                                                                                                                                                                                                                                                                                       60.0%;
                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagner
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                                                                                                           망
                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                           Score 12;
Pred. No.
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                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heas
                                                                                                                                                                                                                                                                  DB 2; Lc...
o. 3.3e+03;
0;
                                                                                                                                                                                                                                                                                                                                                Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; CHD1;
                                                                                                                                                                                                                                                                                                            Length 21;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR
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                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                          Gaps
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Gene expression inhibition method erbB2 gene PCR primer #10.

02-DEC-2004

(first entry)

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RESULT 11
ABI83921
ID ABI83
XX
AC ABI83
XX
DT 15-FF
XX
DE Captı
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                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a DNA methylation inducer (I) containing double-
CC stranded (ds)RNA that targets the region which contains CpG or CpNG (N is
CC A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having
CC DNA that codes dsRNA that targets the region which contains CpG or CpNG
CC which involves introducing (I) is useful in the DNA methylation process,
CC cell is obtained from human. (I) is useful as gene expression inhibitor
CC cell is obtained from human. (I) is useful as gene expression inhibitor
CC cell is obtained from human. (I) is useful as gene expression inhibitor
CC cell is obtained from human. (I) is useful as gene expression inhibitor
CC cell is obtained from human. (I) is useful is gene to the disease related gene
CC cell is obtained from human. (I) is useful for
CC cell is obtained from human. (I) is useful for
CC cell is obtained from human. (I) is useful for
CC cell is obtained from human. (I) is useful for
CC cell is obtained from human. (I) is useful for
CC controlling gene expression, where the disease related gene
CC controlling various biological activities in a mammal by controlling the
CC containing domain on a gene promoter of the target gene, where the
CC containing domain on a gene promoter of the target gene, where the
CC containing domain on a gene promoter of the target gene, where the
CC containing domain on a gene promoter of the target gene.
CC (I) induces sequence specific gene at the expression for the target gene.
CC (I) induces sequence specific gene at the transcription level. (I)
CC mables DNA methylation in the promoter region of a gene, where the
CC gene expression at the transcription of a gene, where the
CC gene expression at the transcription of a gene, where the
CC gene expression at the transcription of a gene, where the
CC gene expression at the transcription level (DNA to mNA). This sequence
CC corresponds to an erbB2 gene PCR primer used in the method to silence
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
Capture oligonucleotide Zip ID#762 oligo #2.
                                                                                                                            ABI83921 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel DNA methylation inducer containing double-stranded RNA targeting region having CpG on DNA in mammalian cell, useful in suppressing gene expression, and as cell growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 60; 98pp; Japanese.
                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-662014/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2004; 2004WO-JP002448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene promoter methylation inducer; cell growth inhibitor; erbB2 gene expression inhibitor; DNA methylation inducer; dsRNA; CpG; human; gene expression; erbB2; tumour; gene transcription; promoter; small interfering RNA; siRNA; gene silencing; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2003; 2003US-0449860P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004076663-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                 4 TIGCCACTCCCA 15
                                                                                                                                                                                                                                                                                                                 l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K, Kawasaki H;
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                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                            TTGCCACTCCCA 2
                                                                                                                                                                                                                                                                                                                                                                                               ВP;
                                                                                                                                                                                                                                                                                                            Conservative
                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                               4 A;
                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                        7 C; 7
                                                                                                                                                                                                                                                                                                                                                      60.0%;
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                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                        G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              Score 12;
Pred. No.
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                                                                                                                                                                                                                                                                                                                       3.3e+03;
                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                           Length 22;
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BXAXAXI
                                                                                                     RESULT 12
ABI83920/c
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                                                                                                                                                                                                                                                                                                             (1) have melting temperatures within a narrow range. The method is useful CC e.g. Salmonella, Listeria monocytogenes and Haemophilus inflectious agents CC infectious agents e.g. Cryptococcus neoformans. Candida albicans and CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus, CC Epstein-Barr virus and polio virus, and parasitic infectious agents CC esteried from Onchoverva volvulus, Entamosba histolytica and Dracunculus CC medinesis. The method is also useful for detecting genetic diseases such CC petecting cancer involving oncogenes, tumour suppressor genes, or genes CC cancer is specifically associated with a gene selected from BRCA1 gene, human papillomavirus types 16 and 18 and liver cancers. The CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The CC and feed industry, detecting comprises scanning (using e.g. a scanning celectron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe consense or absence of the target mucleotide sequences. ABI82074 to of the present invention
                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                 Matches
                         15-FEB-2002
                                                       ABI83920;
                                                                                ABI83920 standard; DNA; 24
                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 25; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; K-ras; PCR primer; probe; capture probe; mutation detection; ligase detection reaction; LDR; p53; BRCA1; Infectious disease; infection; 21 hydroxylase deficiency, Turner Syndrome; obesity; cancer; oncogene; tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary
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                                                                                                                                                                                       1 GCATTGCCACTC 12
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                GCATTGCCACTC 17
                                                                                                                                                                                                                                                                                         24 BP; 5 A; 9 C; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capture oligonucleotide probes for use on a support tary oligonucleotides hybridize with little mismatch.
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zirvi M,
                    (first entry)
                                                                                                                                                                                                                                       60.0%; Score 12;
100.0%; Pred. No.
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                                                                                    ВP
                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                    DB 6; Length 24;
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Capture oligonucleotide Zip ID#762 oligo

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(I) have malting temperatures within a narrow range. The method is useful conditions of the condition of the condition of the condition of the condition to a condition of the conditio
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ABS59154
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BXAXAXB
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method (M1) for designing capture oligonucleotide probes (I) for use on a support to which complements oligonucleotide probes (II) will hybridise with little mismatch, who complements to the probes (II) will hybridise with little mismatch, who complements to the probes (II) will hybridise with little mismatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Designing capture oligonucleotide probes complementary oligonucleotides hybridize
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                  ABS59154 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                al Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 25; 300pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 5 A;
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           5 C;
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                                                                                                                                    ВP
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05-NOV-2002

(first entry)

G-protein

coupled receptor,

probe #101.

Query Match Best Local S Matches 12

1 Similarity
12; Conserv

60.0%; So ilarity 100.0%; I Conservative 0;

Score 12; Pred. No.

DB 6; Lo

Length 26; Indels

Mismatches

0

0

Sequence 26

BP;

7

A; 8 C; 4 G; 7 T; 0 U; 0 Other;

coding

sequences, primers

and

probes

of the

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The invention relates to novel isolated G-protein coupled receptor (GPCR) CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid CC and antibody are useful for treating, preventing or alleviating a GPCR-CC associated disorder or a patchological state in a subject, particularly a CC human. In particular, the disorder is cardiomyopathy, atherosclerosis, CC diabetes, or a disorder related to cell signal processing and metabolic CC pathway modulation. The GPCR polypeptide and mucleic acid are also useful CC for diagnosing the presence of or predisposition to a disease associated CC and polypeptide are especially useful in therapeutic or prophylactic CC applications for disorders associated with abternant GPCR expression or CC treating the above conditions. Furthermore, the nucleic acids and CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate CC ancer, uterus cancer, immune response, neurodegenerative disorders, CC albright hereditary osteodystrophy. These are also useful in developing a CC powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. ABSS9747-ABSS9211 represent human CC GPCP ording arminers and morbes of the invention
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08-FEB-2001;
22-FEB-2001;
14-MAR-2001;
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21-DEC-2000;
04-JAN-2001;
10-JAN-2001;
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Gerlach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis; diabetes; cell signal processing; metabolic pathway modulation; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma; immune response; neurodegenerative disorder; inflammatory disorder; crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                       New G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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19-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page
                                                                                                                                                                                                                                                                                                                                                                                                                           in humans
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Ballinger RA, ...
T. Vernet CAM, Si
Thiston G, S
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2000US-0257876P;
2001US-0259743P;
2001US-0260718P;
2001US-0261498P;
2001US-0263689P;
2001US-0267464P;
2001US-0277946P;
2001US-0277946P;
2001US-0277946P;
2001US-0278150P;
2001US-0285719P;
2001US-0285719P;
2001US-0299327P;
2001US-0399327P;
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                                                                                                                                                                                                                                                                                                                                                                                        568; 685pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             digaru M, Kekuda R,
Shenoy SG, Gusev V,
Stone DJ, Sciore P,
Gangolli EA, Millet
                                                                                                                                                                                                                                                                                                                                                                                           English.
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V, Malyankar UM, Edinger
P, Macdougall JR, Gunther
t I;
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Gunther E;
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04-JAN-2001; 2001US-0259743P.
10-JAN-2001; 2001US-0260718P.
12-JAN-2001; 2001US-0261498P.
24-JAN-2001; 2001US-0263689P.
08-FEB-2001; 2001US-0267464P.
22-FEB-2001; 2001US-0271021P.
14-MAR-2001; 2001US-0278150P.
23-MAR-2001; 2001US-0278150P.
18-APR-2001; 2001US-0284591P.
23-APR-2001; 2001US-0284791P.
19-JUN-2001; 2001US-0289327P.
16-AUG-2001; 2001US-0312902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000;
21-DEC-2000;
04-JAN-2001;
10-JAN-2001;
12-JAN-2001;
ABQ88354 to ABQ88417 represent human G protein coupled receptor (GPCR) cDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins from the present invention. GPCR sequences can have neuroprotective, nootropic, anti-HIV, antiasthmatic, antiarteriosclerotic, cytostatic, immunomodulator, antiinflammatory, antidiabetic, anorectic, haemostatic, antibacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic, cardiant, antiulcer, antiallergic, hepatotropic and antiparkinsonian
                                                                                                                                                                 New isolated human G-protein coupled receptor x (GPCRX) polypeptide, useful for treating or preventing GPCRX-associated disorders e.g. diabetes, atherosclerosis, cancer or obesity.
                                                                                                                                     Example 3; Page 245; 354pp; English.
                                                                                                                                                                                                                                                                  Li L, Padigaru M, Ballinger RA, Keku
Smithson G, Peyman JA, Macdougall JR,
Gunther E, Millet I, Tchernev VT, And
Zhong H, Ellerman KE, Wolenc A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G protein coupled receptor; GPCR; GPCRX; neuroprotective; nootropic; anti-HTV; antiasthmatic; antiarteriosclerotic; cytostatic; immunomodulator; antiinflammatory; antiidabetic; anorectic; haemostatic; antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic; cardiant; antiulcer; antiallergic; hepatotropic; antiparkinsonian; HIV; vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes; metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma; infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer; allergy; cirhosis; glomerulonephritis; stroke; haematopoietic disorder;
                                                                                                                                                                                                                                        WPI; 2002-557660/59.
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Synthetic.
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e D, Vernet CAM, Shenoy
D, Gusev V, Malyankar U
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Matches 12
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22-FEB-2001;
14-MAR-2001;
13-MAR-2001;
18-APR-2001;
 (LILL/)
(PADI/)
(BALL/)
(KEKU/)
(COLM/)
(SPYT/)
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24-JAN-2001;
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04-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                            ss; primer; PCR; human; G-protein coupled receptor; GPCRX; cancer, breast; ovarian cancer; hypercalcaemia; endometriosis; Crohn's disappendicitis; cirrhosis; infertility; cardiovascular disorder; cardiomyopathy; atherosclerosis; autoimmune disease; scleroderma; systemic lupus erythematosus; diabetes; pancreatitis; subjected; pancreatitis; renal disorder; glomerulonephritis; renal tubular acidosis; immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activities, and can be used in vaccines and gene therapy. GPCR proteins, nucleic acid molecules, and antibodies from the present invention can be used for manufacturing a medicament for treating or preventing a GPCR-associated disorder or syndrome related to cell signal processing and metabolic pathway modulation, such as cardinoyopathy, atherosclerosis, diabetes, cancer, obseity, infections (bacterial, fungal, protozoal or viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be used diagnostically to monitor protein levels in tissues as part of a clinical testing procedure such as in determining the efficacy of a given treatment regimen. AB084318 to AB086339 represent PCR primers and probes for the human GPCRs of the present invention
                                                                                                                                                                                                                                       10-JAN-2001;
                                                                                                                                                                                                                                                                               18-DEC-2000;
                                                                                                                                                                                                                                                                                                        19-DEC-2001;
                                                                                                                                                                                                                                                                                                                                      23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI04496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI04496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26
PADIGARU M
BALLINGER I
KEKUDA R.
COLMAN S D
SPYTEK K A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TTGCCACTCCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCCACTCCCA 16
                                                                                                                    2001US-0260718P.

2001US-0261498P.

2001US-0263689P.

2001US-0267464P.

2001US-0271021P.

2001US-0275946P.

2001US-0278150P.

2001US-0284591P.

2001US-0284591P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 7
                                                                                               2001US-0285718P
2001US-0299327P
2001US-0312902P
                                                                                                                                                                                                                                                                                                        2001US-00025806
                                                                                                                                                                                                                                                 2000US-0257876P.
2001US-0259743P.
                                                                                                                                                                                                                                                                              2000US-0256635P
                                    7 X
20 •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 8 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor forward primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPCRX; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                               immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   % proteins,
can be
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RESULT 16
AAV44981/c
ID AAV449
XX
AC AAV449
XX
DT 16-NOV
DT 2X
XX
DE PCR pr
XX
KW Uncoup
                                                                                                                                                                                                                                                               polypeptide. The polypeptide, nucleic acid, antibody, and their CC biologically active derivatives or fragments, are useful in determining the predisposition to or presence of GPCRX-associated disorders or Syndromes and in manufacturing a medicament for treating, diagnosing or CC expreventing the said disorders such as cancer (e.g. breast or ovarian cc cancers), hypercalcaemia, endometriosis, Crohn's disease, appendicitis, CC cirrhosis, infertility, cardiovascular disorders (e.g. cardiomyopathy, CC atherosclerosis), autoimmune diseases (e.g. scleroderma, systemic lupus cerythematosus), diabetes, pancreatitis, Alzheimer's disease, stroke, CC myasthenia gravis, schizophrenia, renal disorders (e.g. cglomerulonephritis, renal tubular acidosis), and/or other similar CC pathologies and disorders. The polypeptides are also useful as immunogens CC to produce antibodies and as vaccines. The present sequence represents a CC GPCR primer of the present invention.
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                                                                                                                                                                                                                          Best
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li L, Padigaru M, Ball:
Casman SJ, Edinger SR,
Macdougall JR, Stone DJ
Tchernev VT, Anderson DJ
Ellerman K, Wolenc AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated GPCRX polypeptide, useful for determining the predisposition to or presence of GPCRX-associated disorders or conditions, and in manufacturing a medicament for treating or preventing diseases such as cancer and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-852781/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ANDE/)
(GUSE/)
(MALY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GERL/)
(SCIO/)
(SEYM/)
(PEYM/)
(MACD/)
(STON/)
(STON/)
(VERN/)
(SHEN/)
(GUNT/)
(MILL/)
(MILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WOLE/)
                        PCR primer
                                                                                                                                                                                                                                                              Sequence
                                                  16-NOV-1998
                                                                          AAV44981;
                                                                                                  AAV44981
                                                                                                                                                                                                                          Local
                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILLET I.
TCHERNEV V T.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CASMAN S J.
EDINGER S R.
GERLACH V.
                                                                                                                                                              s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELLERMAN K. WOLENC A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERNET C
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MALYANKAR U M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMITHSON G. PEYMAN J A.
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZHONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACDOUGALL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIORE P.
                                                                                                                                                                                     TTGCCACTCCCA 15
                                                                                                                                                                                                                                                               26
                                                                                                 standard;
                                                                                                                                                             TTGCCACTCCCA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 257; 221pp; English.
 protein
                        for UCP2 gene transcriptional promoter sequence
                                                                                                                                                                                                                                                              BP; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 paru M. Ballinger RA, Kekuda R. Colman
Edinger SR, Gerlach V. Sciore P. Smit
RR, Stone DJ, Vernet CAM, Shenoy SG, (
Anderson DW, Gusev VY, Malyankar UM,
                                                                                                                                                                                                           Conservative
                                                 (first
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M
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                                                                                                  CDNA; 29
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                                                  entry)
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                                                                                                                                                                                                                                       60.0%;
  UCP2
                                                                                                                                                                                                                                                               C; 4
  gene;
                                                                                                  дB
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                               <u>ი</u>
                                                                                                                                                                                                                          Score 12;
Pred. No.
                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                               T; 0
 transcriptional
                                                                                                                                                                                                                                                               U; O
                                                                                                                                                                                                                           DB 10; I
3.3e+03;
                                                                                                                                                                                                                                                               Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colman SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smithson G, Pe
SG, Gunther E,
ar UM, Zhong H;
                                                                                                                                                                                                                                       Length 26
  promoter; mouse;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spytek KA;
                                                                                                                                                                                                               <u>,,</u>
                                                                                                                                                                                                                                                                                                                 as immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peyman
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Millet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JA;
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RESULT 17
AAV08886/c
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is a PCR primer for the human mitochondrial uncoupling protein 2 (UCP2) gene transcriptional promoter of the invention. The promoter has cis transcriptional regulatory activity. Cells containing the promoter attached to a non-UCP2 gene, in which the non-UCP2 gene is a reporter gene can be used in screening assays for modulators of UCP2 gene expression, which may be useful for treating disorders in which the UCP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondrial protein; cis transcriptional regulatory activity; therapy; expression modulator screening; fat feeding; diabetes; obesity; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                employed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse UCP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-520130/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-1997;
Chen J,
                                                                                                                   Homo
                                                                                                                          Synthetic
                                                                                                                                              UCP2; promoter; therapy; PCR pr
                                                                                                                                                                           PCR primer for UCP2 promoter.
                                                                                                                                                                                              20-MAR-2003
25-FEB-1999
                                                                                                                                                                                                                             AAV08886
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Col 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5807740-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                       25-APR-1997;
                                                                            15-DEC-1998.
                                                                                               US5849514-A.
                                                                                                                                                                                                                                                AAV08886 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TULA-)
                  (TULA-)
                                                        19-JUN-1998;
                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                              upregulated in response to fat feeding, e.g. diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TULARIK INC.
                                                                                                                                                                                                                                                                                                                                                Similarity
                   TULARIK INC
                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amaral
                                                                                                                                                                                                                                                                                                                 TTGCCACTCCCA 15
 Amaral MC
                                                                                                                                                                                                                                                                                                 TTGCCACTCCCA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene promoter - useful for forming transfected cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug
                                                                                                                                                                                                                                                                                                                                                                           BP; 7 A;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                               primer;
                                                                                                                                                                                              (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00846012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00846012.
                                      97US-00846012
                                                          98US-00100297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9pp;
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()
                                                                                                                                                        transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening assays.
                                                                                                                                                                                                                                                cDNA;
                                                                                                                                                                                                                                                                                                                                    100.0%; +-
                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                              ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                 g
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                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                              13 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                 ₽P
                                                                                                                                                                                                                                                                                                                                                 Score 12; DB 2; L
Pred. No. 3.3e+03;
                                                                                                                                                          factor; modulator; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   obesity
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RESULT 18
AAZ28769/
ID AAZ2
XX AAZ2
XX AAZ2
XX O1-F
DE G-le
XX Olig
KW mRNA
KW anti
OS Synt
XX WO95
XX O7-C
XX O7-C
XX O1-F
PD O7-C
XX O1-F
PF 31-F
XX YIU
XX WPI
XX WPI
XX WPI
XX A N
PS Exar
XX A N
PS Exar
XX The
CC The
CC Tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
The oligonucleotides AAZ28763-Z28772 are used in a capture assay for Tatmodulated transcription of guanine (G)-less mRNA expression in viro, following addition of a potential transcriptional activator or inhibitor. The method is used to detect a selected RNA in a sample, comprising: (a) contacting a sample with an oligonucleotide comprising a region complementary to the selected RNA to form an RNA/DNA duplex, (b) cleaving single-stranded RNA in the sample, (c) binding RNA duplex to a sample with an oligonucleotide comprising a region complementary to the selected RNA to form an RNA/DNA duplex to a sample with a contact of the selected RNA to form an RNA/DNA duplex to a sample with a contact of the selected RNA to contact of the select
                                                                                                                                                                                                                                       Example I; Page 40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-610868/52
                                                                                                                                                                                                                                                                                                                                                                                                                    Sivaraja M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TULA-) TULARIK INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9950459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-less oligonucleotide GLESS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antineoplastic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a PCR primer for the UCP2 promoter. The amplified sequence is used in the method of the invention, which is a screening assay for agents that modulate the effect of a transcription factor on a UCP2 promoter comprises combining the promoter and transcription factor in the presence and absence of a candidate agent an determining any change in the effect of the transcription factor on the promoter. The promoter comprises at least 50 nucleotides of a sequence comprising nucleotides 1-460 of the UCP2 promoter (see AAV08879). The method is used to identify agents that modulate UCP2 gene transcription (agents that upregulate UCP2 are potentially useful for treating diabete and obesity). (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ28769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ28769 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nnucleotide; capture assay; tat; modulation; transcription; guanine;
expression; activator; inhibitor; detection; ss; gene expression;
neoplastic; antifungal; antiviral; disease.
                                                                                                                                                                                                                                                                                               method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCCACTCCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assay for modulators of UCP2 on of transcription factor and
                                                                                                                                                                                                                                                                                                                                                                                                                    Strulovici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00052995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US007127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                            RNA in a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                뫋
                                                                                                                                                                                                                                                                                                                                                                                                        Flores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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3.3e+03;
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d defined UCP2 promoter s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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substrate,

standard;

DNA; 51

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RESULT 20
AAI75760/c
ID AAI75760;
XX
AC AAI75760;
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AAL55696/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                     Sequence
                                                                                                                                                                       The invention relates to a novel human zinc finger 32.56 polypeptide, encoding polynucleotide, an antagonist and a method for recombinant production. The polypeptide is useful for treating cancer and HIV infection. The current sequence is that of the human zinc finger 32.5.
                                                                                                                                                                                                                                                                                                            Mao
                                                                                                                                                                                                                                                    New Polypeptide-human zinc finger protein-32.56, encoding polynucleotide, antagonist and recombinant production, useful for treating cancer and
                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                        WPI; 2003-249003/25.
                                                                                                                                                                                                                                                                                                                                              18-APR-2001; 2001CN-00112608.
                                                                                                                                                                                                                                                                                                                                                                   18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-2002.
                                                                                                                                                                                                                                                                                                                               (BIOW-)
                                                                                                                                                                                                                                                                                                                                                                                                        CN1381467-A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL55696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL55696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bound RNA duplex. The invention is used as a high throughput assay identify modulators of gene expression that may serve for example \varepsilon antineoplastic, antifungal or antiviral agents for the treatment of wide variety of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39 BP;
                                                                                                                          Local
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                                                                                                                12;
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                                                                                                                        Similarity
                                                                                      ACTCCCATTCTT 20
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                                                                                                                                                    41 BP; 10
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                                                                                                                                                                                                                             Page 22; Opp;
                                                                                                            60.0%; So larity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             finger 32-56-related probe
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                                                                                                                                                    A; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         32.56; cancer; HIV; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No.
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Pred. No.
                                                                                                                                                G; 14 T; 0 U; 0 Other;
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                                                                                                           3.3e+03;
thes 0;
                                                                                                                               DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                            Length 41;
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                                                                                                           Indels
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finger 32.56-
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RESULT 21
AA175759/c
ID AA1757
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AC AA1757
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DT 09-NOV
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DT 09-NOV
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XX
XX
KW Human;
KW protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999; 99US-0168138P.
29-NOV-2000; 2000US-00726173.
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  Human; single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic nucleic acid sequences, useful in genetic testing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000; 2000WO-US032758
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                                                                         Human silent SNP
                                                                                                                     09-NOV-2001
                                                                                                                                                                                                                  AAI75759 standard; DNA; 51
                                                                                                                                                                                                                                                                                                                                  35
                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                  TGCCACTCCCAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 10
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                                                                                                                     (first entry)
                                                                    containing nucleic acid SEQ:2700.
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hes 0;
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AMI73060 to AAI79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AAM53114 to AAM5329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein cc polynucleotide sequences. The sequences can be used in gene and protein cc therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases cassociated with inappropriate expression of polymorphic polypeptides. For cc example, (I) may be used to treat disorders by rectifying mutations or cd eletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own cc production of polypeptide. Additionally, (I) and its complementary csequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic colypeptides in samples may also be used as diagnostic agents for detecting the presence of polymorphic colypeptides in samples may also be used as diagnostic agents for detecting the presence of polymorphic colypeptides in samples may also be used as diagnostic agents for detecting the presence of polymorphic colypeptides in samples may also be used as diagnostic agents for detecting the presence of polymorphic colypeptides may also be used as diagnostic agents for detecting the presence of polymorphic p
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Best Local :
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29-NOV-2000; 2000US-00726173
                                                                                                            Human; single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic; ds.
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                                                                                                                                                                                                                                                      09-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 877; 2653pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic nucleic acid sequences, useful in genetic testing
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                        WO200140521-A2
                                                                   Homo sapiens.
                                                                                                                                                                                                        Human silent SNP containing nucleic acid SEQ:2699
                                                                                                                                                                                                                                                                                                                                                AAI75758 standard; DNA; 51 BP
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                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12; DB 4; Le Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 51;
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PF XXX C XXX
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AAH38540
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CC AAM53114 to AAM53329 represent peptides related to human polymorphic CC polynucleotide sequences. The sequences can be used in gene and protein CC them may be used in the prevention. (I) and the polypeptides encoded by CC associated with inappropriate expression of polymorphic polypeptides. For CC example, (I) may be used to treat disorders by rectifying mutations or CC deletions in a patient's genome that affect the activity of polypeptides or Dy expressing inactive proteins or to supplement the patients own CC sequences may also be used as DNA probes in diagnostic assays to detect therefore which patients may be in need of restorative therapy. The antibodies specific for polymorphic polypeptides. The antibodies may also be used as antityes. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 12
13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                               Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                 WO200129262-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH38540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH38540 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51 BP; 13 A; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 877; 2653pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-356160/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999; 99US-0168138P
29-NOV-2000; 2000US-00726173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-2000; 2000WO-US032758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2001
                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TGCCACTCCCAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 flanking oligonucleotide SEQ ID 1336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%; Score 12; DB 4; L
100.0%; Pred. No. 3.3e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                        investigation; paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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XX (ORCH-) ORCHID BIOSCIENCES INC.

PX (ORCH-) ORCHID BIOSCIENCES INC.

PX Picoult-Newburg L, Pohl M;

Pi Picoult-Newburg L, Pohl M;

PY absence or identity of single polymucleotide polymorphism in a nucleic Ry wew genotyping oligonucleotide, useful for detecting the presence, pri acid sample.

XX New genotyping oligonucleotide, useful for detecting the presence, pri acid sample.

XX New genotyping oligonucleotide, polymucleotide polymorphism in a nucleic series of single nucleotide polymorphism such a series of regions flanking sequence AAH37205 - AAH40944 represent PCR primers, single nucleotide grimer extension (SNPB) primers, and the sequences of regions flanking sequence, the SNPB primer is used as a genotyping a minimal primer.

XX Sequences AAH37205 - AAH40944 represente or absence of a SNP, using the primer extension control of the support of a SNP flanking the presence or absence of a SNP, using the primer is used as a genotyping primer.

CC oligonucleotides are useful for genotyping a nucleic acid sample by the oligonucleotides are useful for genotyping nucleic acid sample by the oligonucleotides are useful for genotyping primers.

CC performing a single-nucleotide primer extension reaction. The preforming a shaple-nucleotide primer extension reaction. The preforming a shaple-nucleotide primer extension reaction. The preforming a shaple-nucleotide primer is used as a genotyping primer.

CC oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to oligonucleotides are useful. For genotyping represence of an individual or group of caused by one or more SNPs. Phenotypic traits unspected of being agammajobultinamenta, disabetes insipidus, Lesch-Nyhan syndrome, muscular of caused by one or more SNPs. Phenotypic traits include diseases e.g.

CC disabetes imperfects and acute intermittent porphyria. Phenotypic craits also include symptoms of or susceptibility to multifactorial conditions and primer and primer and primer and pri
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RESULT 24
ABL00487/c
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                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                               Query Match
Best Local
    22-NOV-2000; 2000WO-US032311
                                        WO200138586-A2
                                                                             Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; inflammation; cancer; nervous system disease;
                                                                                                                            Human
                                                            Homo sapiens.
                                                                                                                                              05-MAR-2002
                                                                                                                                                                  ABL00487
                                                                                                                                                                                  ABL00487 standard;
                                                                                                                                                                                                                                                                              Local
                                                                                                                      silent noncoding SNP oligonucleotide SEQ
                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                               GCATTGCCACTC 39
                                                                                                                                                                                                                                                GCATTGCCACTC 12
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                  ç.
                                                                                                                                                                                                                                                                          Score 12;
Pred. No.
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                           DB 4; 4; 3.3e+03; 0;
                                                                                                                       ID NO:478
                                                                                                                                                                                                                                                                                Length 51
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                             0
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RESULT 25
ABN44520
ID ABN44520
ID ABN44
XX ABN44
XX ABN44
XX ABN44
XX ABN44
XX Humar
XX Humar
XX Homo
XX Homo
XX HOZOC
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antinicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human spliced transcript detection oligonucleotide SEQ ID NO:17268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN44520 standard; DNA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 392; 674pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-355949/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200210449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN44520
                               WPI; 2002-257383/30
                                                                                                                                                                                                          28-JUL-2000;
02-MAY-2001;
                                                                                                                                                                                                                                                                                               20-JUL-2001; 2001WO-IB001903
                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
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                                                                                       Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse; rat; splice transcript; detection; RNA transcript; variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                  COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATTGCCACTC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATTGCCACTC
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                                                                                       Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leach M;
                                                                                                                                                                                                          2000US-0221607P.
2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 11 C; 15 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%; Score 12;
100.0%; Pred. No.
Live 0; Mismatc
                                                                                          Mintz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 T; 0
                                                                                          Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                             Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Sequence 60 BP; 11 A; 17 C;

13 G; 19 T; 0 U; 0 Other;

0

but was obtained in electronic format

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transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular libraries to detect transcripts of a sub-transcriptome under a particular
                                                and pathology-specific genes such as those genes only expressed in specific tissue under a specific genes fathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                     biological or pathological state, and so allowing the detection of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes oligonuclectide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17268; 47pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                            Human;
splice
                                                                                                                                                                                                                                Human spliced transcript detection oligonucleotide SEQ ID NO:15069.
Shoshan A,
                                                  28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                                      20-JUL-2001; 2001WO-IB001903
                                                                                                                                           WO200210449-A2
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                           15-JUL-2002
                                                                                                                                                                                                                                                                                      ABN42321;
                                                                                                                                                                                                                                                                                                               ABN42321 standard; DNA; 60
                                                                                                                 07-FEB-2002
                           (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                            mouse; rat; splice transcript; detection; RNA transcript; variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 GCATTGCCACTC 12
                                                                                                                                                                                                                                                                                                                                                                                 GCATTGCCACTC 55
 Wasserman
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
 Þ
 Mintz
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
 Ħ
 Mintz
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; LC
. 3.3e+03;
 Ļ
  Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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PT XXX PR X XXX PT XXX

New oligonucleotide libraries comprising oligonucleotides which

WPI; 2002-257383/30

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RESULT 27
ABF27951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcriptome, where the (sub-)transcriptome units that populate a genome. The library comprises several cc oligonucleotides, each capable of hybridising selectively to a set of comessenger RNAs transcribed from multiple cc which encodes one or more messenger RNAs splice variants. The clibraries are useful for detecting mRNAs from a cc quantitatively characterising the corresponding transcriptome, and in cc quantitatively characterising the corresponding transcriptome, and in cc detecting RNA transcripts and splice variants of human or animal cc libraries to detect transcripts of a sub-transcriptome under a particular condition to pathological state, and so allowing the detection of tissue specific tissue under a specific pathological condition; to detect variants of a transcriptome of a batient suffering from a particular cc disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from cc part of the printed specification, but was obtained in electronic format cf the grant invention. N.B. The sequence data for this patent did not format condition from wiffor at the was obtained in electronic format condition to the condition. The sequence data for this patent did not form cc directly from wiffor at the was obtained in electronic format condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 12
Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosin
                                                                                               Olek
                                                                                                                                                       07-APR-2000; 2000DE-01019173
                                                                                                                                                                                  06-APR-2001; 2001WO-IB000713.
                                                                                                                              (EPIG-)
                                                                                                                                                                                                                        18-OCT-2001
                                                                                                                                                                                                                                                         WO200177384-A2
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                    peptide nucleic central nervous
                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABF27951 standard; DNA; 13 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60 BP; 17 A; 11 C; 19 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 15069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selectively hybridize to mRNAs transcr
genome, useful for detecting tissue-,
                                                            2001-657177/75
                                                                                                                                                                                                                                                                                                       single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
ide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
ral nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                         EPIGENOMICS
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RESULT 28
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC00010-ABE39989, ABF00010-ABF39989, ABH00010-ABH39989 and ABI00010-ABH32073 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                    Claim 1; SEQ ID NO 127947;
                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.
                                                                                                                                                                                                                                             WPI; 2001-657177/75.
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                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99389, ABF00010-ABC99389, ABF00010-ABC99389, ABF00010-ABC99389, The oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                data for this patent did not form part of was obtained in electronic format from W ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A,
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Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
                            Canine IL-2
                                                                                  AAV95069;
                                                                                                            AAV95069 standard; RNA; 17
                                                                                                                                                                                                                                                                                             Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
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                           receptor g-chain substrate position 17.
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system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No.
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RESULT 32
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                   (ALKU ) AKZO NOBEL NV
                                                                                                                    Infectious salmon anemia virus
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                                                                                                                                                      Structural
                                                                                                                                                                  ISAV structural protein-1 (SP-1) forward primer.
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21-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                       The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (II)-2R gamma encoded RNA ANV93889 to ANV9576 represent specifically claimed ribozymes, and ANV9575 to ANV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor
                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                               CATTGCCACTC 12
                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 45;
                                                                                                                                  protein-1; SP-1; infectious salmon anaemia virus;
salmon anaemia; ISA; vaccine; virucide; fish; PCR
Кговвоу В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DT,
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                          BP; 4 A;
                                                                                                                                                                                          (revised)
(first entry)
                                      99EP-00203401
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                                                                                                                                                                                                                                                                                                                                            55.0%;
                                                                                                                                                                                                                                                                                                                                                                      8 C; 2 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; hairpin ribozyme; substrate; expression;
psoriasis; allergy; inflammatory disease;
                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin 2 - useful for treating e.g. allergies.
                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                            Score 11; [
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                            DB 2,
1.2e+04;
0;
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                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                             ISAV;
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                                                                                                                                    primer;
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RESULT 33
ABR93931/C
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Matches
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                                                                                                                                                                                                                   treating
pathologi
                                                                                                                                                                                                                      New synthetic ribozyme that cleaves androgen treating prostate hyperplasia or cancer, and pathologies.
                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; androgen receptor; AR; cytostatic; androgen receptor inhibitor; gene therapy; ribozyme; cell proliferation; prostatic cancer cell; prostate hyperplasia; prostate cancer; androgen dependent pathology; se hammerhead ribozyme; HR2; PCR; primer; polylinker; pcDNA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pcDNA3 vector polylinker PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                          (TEXA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX93931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a structural protein-1 (SP-1) of infectious salmon anaemia virus (ISAV). The SP-1 polynucleotide, protein or specific antibodies are useful in diagnostics, and in vaccines to protect fish against infection with ISAV. The SP-1 polynucleotide is useful for producting vector vaccines against the virus, and for recombinant production of SP-1, substantially free from other ISA viral protein. The present sequence represents an oligonucleotide derived from the ISAV SP-1 DNA, that can be used as a primer. (Updated on 11-SEP-2003 to standardise os field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX93931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 5; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide encoding structural protein-1 of infectious salmon anemia virus in vaccine preparation for protecting fish against the viral infection, and in diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                       ĀΚ,
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                                                                                                                                                              38pp;
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                                                                                                                                                                 English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 3 T; 0 U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2e+04;
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                                                                                                                                                                                                                                receptor mRNA, other androgen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathology; ss,
                                                                                                                                                                                                                                useful for dependent
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The invention describes A synthetic ribozyme (I) receptor mRNA. A vector comprising (I) is useful receptor activity in cultured prostate cells, by preparation comprising the vector. The vector is inhibiting the proliferation of prostatic cancer received to the collection of prostatic cancer to the collection of prostation of

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l for reducing androgen
y providing to the cells a
s also useful for
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
Query Match
Best Local
                                                                                                                                                                                                                                                         The invention relates to synthetic ribozyme capable of selectively targeting the androgen receptor mRNA. Also included are a gene encoding the synthetic ribozyme, a vector comprising the gene (where expression of the gene in a human prostatic cancer cell is capable of inhibiting androgen receptor activation), reducing androgen receptor activity in an animal having prostatic hyperplasia by administering a preparation comprising the vector, and treating prostatic hyperplasia by administering to the patient a formulation of an active preparation of a ribozyme gene construct comprising a human promoter sequence in a vector carrier (where the ribozyme gene construct comprises a ribozyme gene that provides an expression product capable of selectively reducing androgen receptor activation). The synthetic ribozyme is capable of selectively reducing of an activation of a receptor activation). The synthetic ribozyme is capable of selectively reducing androgen receptor mRNA and can be used in the inactivation of a receptor gene construction and for treating prostatic hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating prostate hyperplasia or cancer, and other androgen dependent pathologies. This sequence represents a primer used to detect express of hammerhead ribozyme HR2 in cultured cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New synthetic ribozyme capable of selectively targeting androgen receptor mRNA, useful in inactivating androgen receptor gene expression, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-1996;
08-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; ss; androgen receptor; ribozyme; prostatic hyperplasia; prostate cancer; PCR; primer; RT-PCR; reverse transcriptase PCR; pcDNA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA61988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 7; 40pp; English
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                                                                                    Sequence
                                                                                                                                                                                                       androgen receptor gene expression, and for treating prostatic hyperplasia and prostate cancer. The present sequence is reverse transcriptase (RT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA )
                                                                                                                                               designed
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                                                                                                                                                                              primer used to assess ribozyme expression
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                                                                                                                                                  against the vector
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                                                                                          BP; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97US-00853164.
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   55.0%;
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                                                                                          4 C; 7
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                                                                                       G; 4 T; 0 U; 0 Other;
                                                                                                                                               pcDNA3
   Score 11;
Pred. No.
      DB 9; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                              in transfected cells
                               Length 18;
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Local Similarity

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RESULT 35
AAV18643
ID AAV18
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AC AAV18
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AAV80303/c
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Best Local :
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                                                                                                                                                                                                                                                                               Sequence 19 BP; 4 A; 10 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       analysis
                                                                                                                                                                                                                                                                                                                                                                      DNA encoding mammalian BRCA1 associated protein, BAP-1 - useful for, e.g. detecting cancer involving breast and ovarian cancer susceptibility gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1996;
19-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV18643 standard; DNA;
multiple sclerosis; graft rejection; immunodeficiency; HIV;
          apoptosis; lymphocyte; recombinant; medicament; Fas-Ligand; AIDS; CD3/T cell receptor; TCR; intracellular mediator; treatment; tumour inflammation; acute hepatitis; autoimmune disease; diabetes; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-145723/13.
                                                                                                                                                                                                                                                                                                                                                                                                                             Rauscher FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9805968-A1
                                             Glucocorticoid-induced leucine-zipper family related
                                                                  Murine GILR cDNA specific reverse primer.
                                                                                        16-FEB-1999
                                                                                                              AAV80303;
                                                                                                                                    AAV80303
                                                                                                                                                                                                                                                                                                    The sequence is that of a PCR primer which was used analysis of BAP-1 (BRCA1 associated protein) cDNA
                                                                                                                                                                                                                                                                                                                                        Example 8;
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                                                                                                                                                                                                                                    Local Similarity
nes 11; Conserv
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                                                                                                                                   standard; DNA; 20
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                                                                                                                                                                                           CCACTCCCATT
                                                                                                                                                                                                                                                                                                                                        Page 45; 100pp; English.
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                                                                                        (first entry)
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97US-0038109P.
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                                                                                                                                                                                                                                                 Score 11;
Pred. No.
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                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                 1.2e+04;
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                                                                                                                                                                                                                                                            Length 19;
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                                              protein;
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     detection;
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                          tumour;
                                               GILR;
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RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
hVR3; vanilloid receptor; dorsal root ganglia; chromosome 12; capsaicin; marker D12S197B; marker D12S1893; nociceptor; calcium; influx; inhibitor; modulator; analgesic; uropathic; anti-rheumatic; anti-arthritic; neuropathic; cerebroprotective; vasotropic; anti-asthmatic; anti-inflammatory; anti-migraine; primer; ss.
                                                                                                                                                               Sense primer for hVR3 3' DNA amplification.
                                                                                                                                                                                                                                12-SEP-2000
                                                                                                                                                                                                                                                                                                                                 AAA29200 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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CC Human VR1 is preferentially expressed in human dorsal root ganglia (DRG) CC and relative to hVR3 has the highest sequence homology with the rat VR1. CC The hVR3 gene maps to chromosome 12 near markers D12S177E and D12S1893. CC hVR1 is activated by capsaicin, the irritant in hot peppers. VRs are CC back to pain-processing centres in the central nervous system. They are CC also sites for the release of pro-inflammatory mediators in the CC periphery. Capsaicin induces a flux of cations in DRG. The actions of CC capsaicin (excitation/desensitisation) are mediated by VRs. The natural CC hVR sub-types may provide targets for the development of novel analgesic CC agents and agents which may interact with other disorders. hVR is useful CC of hVR activity, e.g. pain, neuropathic pain, inflammatory pain, chronic CC meuralgia, algesia, neurodegeneration, nerve injury, stroke, ischaemia, CC chronic obstructive pulmonary disease (COPD), urological disorder, asthma, CC chronic obstructive pulmonary disease (COPD), urological disorder, asthma, CC disorder in a human patient (claimed)
          Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                       Human vanilloid receptor protein or its variant useful for treating preventing a disorder responsive to the modulation of hVR activity, as pain, neuropathies, neuralgia, algesia, neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 28; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1998;
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       ВP;
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       2 A;
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7 C; 4 G; 7 T; 0 U; 0 Other;
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Query Match Best Local Similarity Matches 11, Conservative 100.0%; 55.0%; <u>,,</u> Score 11; Pred. No. Mismatches DB 3; 1.2e+04 Length 20 Indels 0; Gaps

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RESULT 38
ADA74107
ID ADA74
XX ADA74
AC ADA74
XX 20-NO
XX Equin
XX Horse
XX Prime
XX Equus
XX Equus
XX Equus
XX Squus
XX 1-JU
XX 1-JU 20-NOV-2003 ADA74107; (first entry)

ADA74107 standard; DNA;

20

Equine laminin gamma-2 cDNA PCR primer #16

Horse; PCR; 88; laminin gamma-2; junctional epidermolysis bullosa; JEB,

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US2003143545-A1 Equus caballus

31-JUL-2003

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RESULT 39
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the equine laminin gamma-2 polypeptide and the polynucleotide encoding it. The invention also relates to a method for diagnosing junctional epidermolysis bullosa (JEB) in a horse, comprising obtaining a biological sample from the horse, isolating DNA and amplifying the DNA encoding laminin gamma-2 using appropriate primers and analysing the amplified nucleic acid to identify the presence of a mutation, where the homozygous presence of the mutated nucleic acid encoding laminin gamma-2 indicates the presence of epidermolysis bullosa. Alternatively, the protein component from the sample can be isolated and screened for laminin gamma-2, where the absence of laminin gamma-2 nucleic acids, proteins and antibodies against the proteins are useful for diagnosing JEB in horses. This sequence represents a PCR primer used to amplify cDNA encoding equine laminin gamma-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated equine laminin polynucleotide, useful for c
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002;
                                                                                                                                                                                food testing; allergen; PCR primer; Fagopyrum esculentum
major allergenic storage protein; FAGAG1; ss.
                                                                                                                                                                                                                   Major allergenic storage protein FAGAG1 PCR primer FAG22
                                                                                                                                                                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                                                            ADA24256 standard; DNA;
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                                                                                                                      WO2003068964-A1
                                                                                                                                            Fagopyrum esculentum.
 Yamakawa
                                                                    26-SEP-2002; 2002WO-JP009982
                                                                                              21-AUG-2003
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                      (NISS ) NISSHIN SEIFUN GROUP INC.
                                               15-FEB-2002; 2002JP-00038930
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11; Conserv
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SPIRITO F.
CHARLESWORTH
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LINDER K.
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No
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 Hayakawa
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RESULT 40
ADI57250/c
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                                                                                                                                                                                                                                                                                                                                                                          drug sensitivity; anti-cancer drug; cancer thera cancer cell detection; indolocarbozole compound;
                                                                                                                                                                                                                                                                                                                                                                                                        drug transport capability; polymorphism; ABCG2; polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 10; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-637145/60.
                                                                                                                                                                                                                                                                                                                      ABC transporter superfamily;
ATP-binding cassette transporter superfamily;
single nucleotide polymorphism; SNP; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI57250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI57250 standard; DNA;
                                                                                                                                                   17-JUN-2002;
                                                                                                                                                                                 13-JUN-2003; 2003WO-JP007534.
                                                                                                                                                                                                                                                      WO2003107249-A1
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-2004
                                                                                                                   (BANY ) BANYU PHARM CO LTD.
                                                                                                                                                                                                                      24-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 CTCCCATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCCATTCTT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 1 A; 11 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           cassette transporter ABCG2 SNP primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                     2002JP-00175806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; but
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11; DB 9; L
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                             therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20
                                                                                                                                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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predicting drug transport capability of mammalian cell by collecting sample from mammal, determining polymorphism of nucleotide sequence of

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Kotani H,

Mizuarai

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2004-156349/15

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RESULT 41
ADK96200/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC capability of a mammalian cell involving collecting a drug transport CC capability of a mammalian cell involving collecting a sample from a CC gene or a polymorphism of the amino acid sequence of ABCG2 polypoptide. CC mammalian cell. Polymuclectides comprising gingle nucleotide companies of the method is useful for predicting drug transport capability of a CC polymorphism of the amino acid sequence of ABCG2 polypoptide. CC mammalian cell. Polymuclectides comprising polymorphic mutations of the CC polypoptides or polypoptides comprising pingle nucleotide or polymorphisms or polypoptides comprising polymorphic mutations of the CC polypoptides, where the subject having the polymuclectides or CC polypoptide is suggested to be sensitive to the indolocarbozole compound. CC measuring drug transport capability. By predicting drug transport capability by protein mutant is useful for CC apability of a mammalian cell, sensitivity of a patient to various drugs can be obtained. As a result of selecting an anti-cancer drugs can be diagnosed and an indicator for the CC cancer therapy and, particularly, detecting a cancer cell(s) which is cellectively apply the compounds for the therapy. In addition, the optimum compounds is reduced whereby a provided. This sequence represents a primer used to identify ans sequence compounds is reduced whereby a provided. This sequence represents a primer used to identify ans sequence compounds is a provided. This sequence represents a primer used to identify ans sequence compounds is compounds in the cancer charapy in sequence capability and the indolocarbozole compounds is reduced whereby and compounds is compounds is sequence represents a primer used to identify ans sequence cancer therapy and the indolocarbozole compounds is compounds is compounded in the cancer therapy and the compounds is compounded in the cancer therapy and the compounds is compounded in the cancer therapy and the compounds is compounded in the cancer therapy and the compounds is compounded to identify and sequence c
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Best Local S
Matches 11
Claim 2; SEQ ID NO 5229; 2627pp; Japanese
                                     Novel polynucleotide useful for PCR amplification along with two fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
                                                                                                                                                  WPI; 2004-093977/10.
                                                                                                                                                                                                                                                                                     08-MAR-2002; 2002JP-00064373
                                                                                                                                                                                                                                          08-MAR-2002; 2002JP-00064373
                                                                                                                                                                                               (KAGA-) KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                       JP2003259875-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK96200 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK96200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 11 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABCG2 gene or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11arity 100.0%; Sometive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide polymorphism; SNP; ss; primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention #1920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                  GIJUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymorphism of amino acid sequence of ABCG2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                       SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 11; DB
%; Pred. No. 1.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 20
1.2e+04;
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Best Local
The invention relates to a new compound 8-80 nucleobases in length (an antisense oligonucleotide) targeted to a nucleic acid molecule encoding forkhead box C2, where the compound specifically hybridises with the nucleic acid molecule encoding human forkhead box C2 appearing as ADN31339 and inhibits the expression of forkhead box C2. Also included
                                                                                       New compound targeted to a nucleic acid molecule encoding forkhead C2, useful in diagnosing and treating developmental disorder.
                                                                         Example 15; SEQ ID NO
                                                                                                                                                        Dobie KW,
                                                                                                                                                                                               21-NOV-2002; 2002US-00303635
                                                                                                                                                                                                                     21-NOV-2002; 2002US-00303635
                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                      US2004102621-A1
                                                                                                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                                      modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                            modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; antisense; forkhead box C2; developmental disorder. lympoedema; lympoedema-distichiasis; dysgenesis; iridocorneal Axenfeld-Rieger anomaly; congenital glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human forkhead box C2 antisense oligonucleotide ISI8227187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN31407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a polynucleotide isolated from a gene and is useful for detecting a single nucleotide polymorphism human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN31407 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                 2004-399740/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGCCACTCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGCCACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                          /note= "
                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phosphorothioate backbone and
-methylcytidines"
                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "2'-methoxyethyl
                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   moa
                                                                                                                                                                                                                                                                                                                                                                                                         mod base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                      72; 80pp; English
                                                                                                                                                                                                                                                                                                                                                 _base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                   "2'-methoxyethyl
                                                                                                                                                                                                                                                                                                                 ი
                                                                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                       residue'
                                                                                                                                                                                                                                                                                                                                   residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                         a11
                                                                                                                                                                                                                                                                                                                                                                                       cytidines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
in a
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RESULT 43
ADN89393
ID ADN89
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are inhibiting the expression of forkhead box C2 in cells or tissues, screening for a modulator of forkhead box C2, a diagnostic method for identifying a disease state, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with forkhead box C2. The compound and methods are useful in diagnosing and treating developmental disorders e.g. lympoedemas such as lympoedema-distichiasis, dysgeneses of the mouse iridocorneal angle similar to those seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The present sequence is an antisense oligonucleotide targeting forkhead box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; human; antisense therapy; CD24; hyperproliferative disorder; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human CD24 antisense oligonucleotide #72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN89393;
                                                                                                                                                                                                                          19-NOV-2002; 2002US-00300236.
                                                                                                                                                                                                                                                                              US2004097448-A1.
                                                                                                                                                                                                                                                                                                                                             modified_base
                                                                                                                                                                                                                                                                                                                                                                                              modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN89393 standard; DNA; 20
                                                                                                                                                                                                                                                    20-MAY-2004.
            The
                                       Example 15; SEQ ID NO 83;
                                                                hyperproliferative
                                                                            New compounds, particularly oligonucleotides targeted to a nucleic acid encoding CD24, useful for treating diseases associated with CD24, e.g.
                                                                                                                      WPI; 2004-389189/36.
                                                                                                                                                                                                19-NOV-2002;
                                                                                                                                                                         (ISIS-) ISIS
invention relates to antisense oligonucleotides which are targeted and inhibit the expression of, nucleic acid encoding human {\rm CD24.} The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 BP; 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTGCCACTC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTGCCACTC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                 2002US-00300236.
                                                                                                                                                                         PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                           /mod_base= Other
/note= "2'-methoxyethyl (2'-MOE)
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                              methylcytidines."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          /mod_base= Other
/note= "Phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                      mod_base= Other
                                                                   disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 C; 4
                                                                                                                                                                                                                                                                                                          "2'-methoxyethyl (2'-MOE)
                                      49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11; DB 12;
Pred. No. 1.2e+04;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                        nucleotides"
                                                                                                                                                                                                                                                                                                                                                              nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 45
AAA91279/c
ID AAA912
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AC AAA912
XX

standard;

DNA;

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AAA91279; AAA91279

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RESULT 44
AAQ76368/c
ID AAQ763
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Best Local S
Matches 11
                                          Matches
                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense oligonucleotides are useful for treating a disease or condition associated with CD24, such as a hyperproliferative disorder. They are also useful in research and diagnostics for modulating the expression of CD24. The present sequence represents a human CD24 antisense oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        Epsilon CH4; IgE; immunoglobulin; diagnosis; therapy; hypersensitivity; oligonucleotide; DNA primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ76368 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Saxon A,
                                                                                                                                                                                                                                                                                                                         29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide DNA primer 7 to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ76368;
                                                                                   Sequence 21
                                                                                                                                                                          New IgE isoforms and nucleic acid sequences for diagnosis and treatment of IgE-mediated
                                                                                                                                                                                                             WPI; 1994-316938/39.
                                                                                                                                                                                                                                                                             24-MAR-1993;
                                                                                                                                                                                                                                                                                                   24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                              WO9421676-A1
                                                                                                         This primer was designed to detect human IgE (epsilon) mRNA membrane exon sequences. (Updated on 25-MAR-2003 to correct
                                                                                                                                           Disclosure; Page 15; 45pp; English
                                                                                                                                                                  conditions.
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06-AUG-2003 08-MAY-2001

(revised) (first entry)

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Search completed: September 14, 2005, 10:19:43 Job time: 379 secs
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                                                                                                                                                                                                                                                    This sequence represents a primer used to isolate the grapevine leafroll C virus (GLRaV-5) DNA sequence of the invention. The DNA sequence can be used in an expression construct. The construct is useful for providing c resistance to GLRaV infection in a recombinant plant cell by transforming the plant cell with it, where transcription of the polynucleotide sequence interferes with a normal viral function such as movement, c encapsidation or replication of viral RNA. The polynucleotide sequence is expressed as an antisense sequence and encodes a GLRaV coat protein, c preferably a defective GLRaV coat protein or a GLRaV coat protein. The GLRaV-5 DNA is useful for the synthesis of GLRaV, as c diagnostics and probes, for viral gene mapping and for induced plant GL disease resistance. It is also useful to detect and quantitate expression of GLRaV in plant tissue prior to use in vegetative propagation, by detecting the presence of GLRAV RNA. (Updated on 06-AUG-2003 to correct of GLRAV in plant tissue prior to use in vegetative propagation, by GLRAV in plant tissue prior to use in vegetative propagation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLRaV-5; grapevine leafroll virus; GLRaV infection; GLRaV coat protein; GLRaV HSP70 homologue protein; viral gene mapping; PCR primer; plant disease resistance; ss.
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## ALIGNMENTS

JOURNAL COMMENT RESULT 1 AZ456041/c LOCUS REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION FEATURES DEFINITION KEYWORDS TITLE source Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0258 row: J column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 69.
Location/Qualifiers 1M0258J10R Mouse 10kb plasmid L clone UUGC1M0258J10 R, genomic AZ456041 plasmid inserts Unpublished (2000) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 69) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., Mouse whole genome scaffolding with paired end reads from 10kb Mus musculus Tel: 801 585 5606 Fax: 801 585 7177 Mus musculus (house mouse) AZ456041.1 GI:10614166 AZ456041 USA /lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PDD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource /organism="Mus musculus" /mol\_type="genomic DNA" /strain="C57BL/6J" /db\_xref="taxon:1000" (http://www.jax.org/resources/documents/dnares/). The DNA 'sex="Male" clone="UUGC1M0258J10" 69 bp DNA
d UUGCIM library Mus
nic survey sequence. 0.00 Duval, B., Hamil, C., linear 20 S. from the Jackson musculus genomic 2030 E., SLC, GSS 04-0CT-2000 S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
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KEYWORDS

TITLE

В ঠ ORIGIN

FEATURES

JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL

COMMENT

PUBMED REFERENCE AUTHORS

JOURNAL MEDLINE

TITLE AUTHORS

TITLE

JOURNAL MEDLINE PUBMED REFERENCE

REFERENCE AUTHORS TITLE

ACCESSION VERSION

KEYWORDS

RESULT 3 BX894771

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SOURCE
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Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-planck-Institut fuer
Submitted (31-MAR-2004) Weisshaar B., Max-planck-Institut fuer
Suechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5g22840.

Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MpI
for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated
                                                                                                                                                                                                                                                                                                                                                                                       High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. Weisshaar,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSBO,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weisshaar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics 19 (11), 1441-1442 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12874060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana T-DNA flanking sequence GK-683C03-023156, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. I-Kat SimpleSearch: a flanking sequence tag (FST) database identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of public (31/4732114/gb/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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100.0%; Pred. No. 3.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: I column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Class: plasmid ends
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ828663 22 bp DNA linear GSS 20-FEB-200
2M0105I14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105I14 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
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www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg., 20 S. 2030
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/clone="GK-683C03-023158"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/clome_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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|mol_type="genomic DNA"
                                                                    'sex="Male"
                                                                                         /clone="UUGC2M0105I14"
                                                                                                                                                                             organism="Mus musculus"
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100.0%; Pred. No. 4e-
tive 0; Mismatches
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4e+03;
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AZ658622
LOCUS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                Helia ( ) 5606
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: farith: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CCACTCCCATTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ658622 25 bp DNA linear GSS 14-DEC-200
1M0535F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0535F04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                              Insert Length: 10000 Std Error: (Plate: 0535 row: F column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                     High quality sequence stop: 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWNA2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:1000"
/clone="UUGC1M0535F04"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                        sex="Male
                                                                                                                                                                                                                  organism="Mus musculus
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; Pred. No. 1.4e+04;
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FEATURES

COMMENT

TITLE

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RESULT 6
TA244G07P/c
  Query Match
Best Local Similarity
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                    nhi@sanger.ac.w.

Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruced (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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Trypanosoma brucei
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                                                                                                    /mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="244g07"
                                                                                                                                                                                                               organism="Trypanosoma brucei"
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  60.0%;
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  Score 12;
Pred. No.
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                 DB_9; Length 38;
1.5e+04;
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244g07, forward sequence,
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REFERENCE AUTHORS

TITLE JOURNAL

SOURCE ORGANISM

**EYWORDS** ACCESSION DEFINITION 밁 δ

ORIGIN

COMMENT

ORIGIN

Query Match Best Local Similarity

60.0%;

Score 12; Pred. No.

DB 8; Length 42; 1.5e+04;

FEATURES

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AZ818778/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0089 row: E column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 42.
Location/Qualifiers
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Weisser, R. Stokes, R. Weisser, A. and Wright, D., Weiss, R. Wouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ818778 42 bp DNA linear GSS 20-FEB-20-2M0089E06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0089E06 F, genomic survey sequence.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative funducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XL10-Gold, T1-resistant, P-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eiomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC2M0089E06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male"
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RESULT 8
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Query Match
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Islam, H., Longacre, S., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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GSS.
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clone UUGC1M0169G03 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: G column: 03
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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Mammalia; Eutheria; Rodentia;
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igh quality sequence stop: 45.
Location/Qualifiers
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                                                                          was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCiM library" /note="Vector: pW042nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="UUGC1M0169G03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
  100.0%;
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  Score 12; DB 8; Length 45; Pred. No. 1.5e+04;
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AA276119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vc36e11.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:776684 similar to SW:NU4M_MOUSE P03911 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CCACTCCCATTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28m13 rev2 ET from Amersham High quality sequence stp: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 55)
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                                         8 CACTCCCATTCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
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  CACTCCCATTCT 32
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                                                                                   Conservative
                                                                                                                                                                                                         Library constructed by Bob Barstead."
                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'mol_type="mRNA"
'strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:776684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10090"
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                                                                              60.0%; Score 12; DB 1; Length 55; 100.0%; Pred. No. 1.5e+04; tive 0; Mismatches 0; Indels
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                                                                                    Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R. Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the state of the state 
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                            This is single pass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; sosids; eurosids, II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                          Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ663993 57 bp DNA linear GSS SALK 027603.43.05.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 027603.43.05.x,
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Arabidopsis thaliana
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Characteristics of the Lotus japonicus Gene Repertoire Deduced from Large-Scale Expressed Sequence Tag (EST) Analysis Plant Mol. Biol. 54 (3), 405-414 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota; viridiglantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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BP080931.1 GI:45637592
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                                                               ecker@salk.edu
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/clone_lib="Lotus japonicus roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lotus corniculatus var.
/mol_type="mRNA"
/isolate="Miyakojima MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:34305"
/clone="MR064f09_f"
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; Pred. No. 1.5e+C
0; Mismatches
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          recovered from the left border of
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VERSION
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A., Walker, M., Williams, E.M. and Trask, B.J.
Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels
Genome Biol. 4 (11), R71.1-R71.15 (2003)
                                                                                                                                                                                                                                                                                                                                                 Email: jayoung@fhcrc.org
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ATTGCCACTCCC 29
                                                                                                                                                                                                                                                                                                                                                                                            Tel: 206 667 1471
Fax: 206 667 6524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB173531 59 bp mRNA linear EST 09-OCT-201 OR_2028E03_010501.y1 Adult mouse olfactory epithelium library Mus musculus cDNA clone 2028E03 5', mRNA sequence.
CB173531 CB173531.1 GI:37592160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Young JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Class: TDNA tagged
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  /Clone lib "Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector:
LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by LeslTe Vosshall. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."
                                                                                                                                                                   tissue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2o28E03"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://sigmal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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Pred. No.
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RESULT 13
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center University of Utah
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AZ594221.1 GI:11716327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1M0406K03F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0406K03 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0406 row: K column: 03
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801 585 7177
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                                                                                                                                     Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pND42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                             purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PM042nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0406K03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Male"
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ORGANISM
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AA870012/c
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VERSION
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Best Local
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    67 ACTCCCATTCTT 56
                                              9
                                                                                       12;
                                                                                                             Similarity
                                              ACTCCCATTCTT 20
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Best Local Similarity 100.0%; Pred. No. 1.5e+04; Matches 12; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 70)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CCACTCCCATTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:600102
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Fax: 314 286 1810
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                                                                          /mol type="mRNA"
/db xref="taxon:1090"
/clone="MAGE:1093870"
/cell line="C2C12 (undifferentiated)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
Score 12; DB 1; Length 70; 
; Pred. No. 1.5e+04;
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Conservative

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Mismatches

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BG237192
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        19
                                                                       5 TGCCACTCCCAT 16
                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Putative full
length read vector to vector length is 71 This clone is available
through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 US
(phone: 800 423 4163; email: info@biogeneticservices.com).
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Fax: 314 286 1810
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Sreptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watcrston, R. and Wilson, R., Watcrston, R., Pape, D., Harvey, N., Pape, D., Harvey, N., McCann, R., Watcrston, R., and Wilson, R., Vacann, R., Watcrston, R., Pape, D., Harvey, N., Pape, D., Harvey, N., Pape, D., Harvey, N., McCann, R., Watcrston, R., and Wilson, R., Watcrston, R., Pape, D., Harvey, N., Pape, D., Har
TGCCACTCCCAT 30
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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Shoemaker, R., Keim
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jnpublished (1999)
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                         /clone_lib="Gm-cl071"
/clone_lib="Gm-cl071"
/note="Vector: psport1; Site_1: Not1; Site_2: Sal1; The cDNA library was constructed from mRNA isolated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies psuperscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restrictions site. Sal1 linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments site of the psport1 vector. The ligated cDNA fragments site of the psport1 vector. The ligated cDNA fragments site of the psport1 vector. The ligated cDNA fragments site of the psport1 vector. The ligated cDNA fragments were transformed into E.col1 ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vockin by Anu Khanna at the University of Illinios at Urbana-Champaign. email: 1-vodkin@uiuc.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="GENOME SYSTEMS CLONE ID: Gm-c1071-719"
/tissue_type="immature pods (~2cm long) of greenhouse
grown plants"
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/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
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                                                                                                                                                                                                    60.0%;
                                                                                                                                                            0;
                                                                                                                                                                                                    Score 12;
Pred. No.
                                                                                                                                                            Mismatches
                                                                                                                                                                                       DB 4; Le
1.5e+04;
                                                                                                                                                                                                                               Length 70;
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REFERENCE
AUTHORS
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ORGANISM
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ACCESSION
VERSION
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BU494033/c
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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BX991911/c
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (dog)

Canis familiaris

Canis familiaris

Canis familiaris

Canis familiaris

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Crania;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 74)

Virgin,S., Tianxiang,S., Karst,S., Wobus,C., Lay,M., Clifton,S.,

Pape,D., Marra,M., Hiller,L., Mattin,J., Wylie,T., Dante,M.,

Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J.,

Ronko,I., Tsagareishvili,R., Maguire,L., Kennedy,S., Waterston,R.
                                                                                                                                                                                                           RNA Expression in Diseased Tissues by RDA Unpublished (2002)
Other_ESTs: vaa04e11.x2
Contact: Skip Virgin
RNA Expression in Diseased Tissues by RDA Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                         Email: est@watson.wustl.edu
Library was constructed by Tianxiang Shen and Skip Virgin DNA
sequencing by: Washington University Genome Sequencing Center
information on obtaining a clone please contact: Skip Virgin
(virgin@immunology.wustl.edu)
Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 TGCCACTCCCAT 10
                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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EST.
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vaa04e11.y2 SV DOGRDA RD3
BU494033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams D.J., Biggs, P.J., Cox, A.V., Jonkers, J., Smith, J., Plumb, R.W., Rogers, J. and Bradley, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forward strand read from insert in chromosome engineering clone MHPP38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX991911.1 GI:49723369
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                                        r: -40RP from Gibco.
Location/Qualifiers
organism="Canis familiaris"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP384e03"
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100.0%; Pred. No. 1.6e+04;
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familiaris cDNA 5',
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Taylor,R.G., Nishijima,I., Yu,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA linear Transcription targeting (A4e03, genomic survey sequen
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76 bp mRNA linear EST 04-JUN-1996 md54b04.rl Soares mouse embryo NbMEI3.5 14.5 Mus musculus cDNA clone IMAGE:372175 5' similar to PIR:S54157 S54157 extensin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 76)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein - cowpea;,
W57143
W57143.1 GI:1359002
                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality Possible reversed clone: similarity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
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The WashU-HHMI Mouse EST Project
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Mus musculus (house mouse)
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314 286 1810
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/rote="Vector: pCR2.1-TOPO; PCR products were directly
/note="Vector: pCR2.1-TOPO; PCR products were directly
cloned into TA cloning vector (pre-cut vector pCR2.1-TOPO
was purchased from Invitrogen) Average insert size is
300bp. Our Insert also have same adaptor sequence on both
ends. The sequence of the adaptor is:
5'-ATACGTGCAGGCTGGTTACATCTG-3'."
                /clone lib="Soares mouse embryo NbMEI3.5 14.5"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker, Site 1: Not I; Site 2: Eco RI; lst strand was primed with a Not I oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Brain from a dog with encephalitis"
/lab_host="DH5a"
                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:372175"
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/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                   sex="unknown"
                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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100.0%; Pred. No. 1.6e+04;
cive 0; Mismatches 0;
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                                                                                                                                                                                                                                              61 TGCCACTCCCAT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nadimidata., Tombolan, L., Kronnie, G., Romualdi, C., Vitulo, N., DePitta, C., Tombolan, L., Kronnie, G., Romualdi, C., Vitulo, N., Basso, G. and Lanfranchi, G.
A leukemia-enriched cDNA microarray platform identified new
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 19)
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                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                              clone UUGC1M0194M12
AZ418201
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University of Padova
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Unpublished (2004)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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AJ714048 LKPD01 Homo sapiens
                                                                                                                            1M0194M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0194M12 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: DePitta C
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                                                Mus musculus
                                                              Mus musculus (house mouse)
                                                                                                 AZ418201.1
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                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="bone_marrow"
/clone_Tib="LKPD01"
/note="caucasian"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LKPD02463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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AUTHORS

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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
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Insert Length: 10000 Std Error: 0
Plate: 0194 row: M column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19
Location/Qualifiers
                                                                                                                                                                            AZ822954.1 GI:12992862
                                                                                                                                                                                                                       2M0096I10R Mouse 10kb plasmid clone_UUGC2M0096I10 R, genomic
                                                                                                               Mus musculus
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                      CICCCATICIT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center University of Utah
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Unpublished (2000)
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:: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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100.0%; Pred. No. 5.4e+04;
cive 0; Mismatches 0;
                                                                                                                                                                                                                    genomic survey sequence.
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smid UUGC1M library Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                        AZ967656 19 bp
2M0238M09R Mouse 10kb plasmid UI
clone UUGC2M0238M09 R, genomic &
                                                                                                                                 AZ967656
AZ967656.1 GI:13838883
GSS.
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Unpublished (2000)
Contact: Robert B. William Contact of Utah Continersity of Utah Controlly of Utah
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Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: I column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       CCACTCCCATT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Nouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were adaptored DNA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative of pwass (gil4732114/gb/RF129072.1), a copy-number inductible derivative of plasmid R1. The vector was ligated burified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone="UUGC2M0096I10"
/sex="Male"
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/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                         AZ427595 27 bp DNA linear GSS 03-OCT-2011M0209507R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0209G07 R, genomic survey sequence.

AZ427595 AZ427595.1 GI:10551608
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 27)
                                                              Mus musculus (house mouse)
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Insert Length: 10000 Std Err
Plate: 0238 row: M column: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and
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'strain="C57BL/6J"
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Pred. No. 5.4e+04;
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Welss,R.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0209 row: G column: 07
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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1 (bases 1 to 28)
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                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                     GI:11737934
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Pred. No. 5.
0; Mismatches
                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 40)
                                                                                                                                                                     100193114R Mouse 10kb plasmid clone UUGC1M0193114 R, genomic AZ417928
                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                  7 CCACTCCCATT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Imail: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error:
Plate: 0445 row: B column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Location/Qualifiers
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resources documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored DNA was annealed to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0445B15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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100.0%; Pred. No. 5.5e+04;
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mid UUGC1M library Mus musculus genomic
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Eukaryota; Metazoa;
Mammalia; Eutheria;
l (bases 1 to 47)
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1M0569013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0569013 F, genomic survey seguence.

AZ769040

AZ769040.1 GI:12888765

GSS.
                                                                           Mus musculus (house mouse)
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Insert Length: 10000 Std Error: 0.00
Plate: 0193 row: L column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah
University of Utah
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801 585 7177
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/clone="UUGC1M0193L14"
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/strain="C57BL/6J"
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             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 5.7e+04;
0; Mismatches 0;
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Insert Length: 10000 Std Error:
Plate: 0569 row: O column: 13
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                    AU103440.1 GI:13552961
EST.
                                                                                                                                        AU103440 Sugano Homo sapiens HEP01378, mRNA sequence.
                                                              Homo sapiens
                                                                               Homo sapiens (human)
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gil4732114|gb)AF129072.ll, a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jaj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Suzuki,Y., Construction and characterization of a full
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                                                                                                                                                                                                                    Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                           Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: Ysuzuki@ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP01378"
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                                                            organism="Homo sapiens"
/mol_type="mRNA"
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clone_lib="Sugano Homo sapiens cDNA library"
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     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200
                                                                                                          Homo sapiens
                                                                                                                          Homo sapiens (human)
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HEP03842, mRNA sequence.
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AU103445 GI:13552966
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/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                                                                                                                                                                                    Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 54)
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
MCArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 TIGCCÁCTCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malus x domestica (cultivated apple) Malus x domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN868714 54 bp
001116AAQAA002279HT (AAQA) Royal
clone AAQA002279, mRNA sequence.
CN868714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshiromo-Nakagawa.K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.
L1; Conservative
                                                                     /clone_lib="(AAOA) Royal Gala phloem"
/note="Vector: pBluescript SK(-); Library
Genesis Research & Development"
                                                                                                                                                                 /organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAOA002279"
                                                                                                                                             /tissue_type="Phloem, scrapings from inside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano Homo sapiens cDNA library"
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/db_xref="taxon:9606"
/clone="HEP05740"
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100.0%; Pred. No. 5.8e+04;
7ative 0; Mismatches 0;
   55.0%;
100.0%;
Score 11;
Pred. No.
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Gala phloem
 DB 7; Length 54; 5.8e+04;
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EST 03-JUN-2004 domestica cDNA

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AUTHORS
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CB274124
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Matches
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IMACE:6448532 5', mRNA sequence.
CB274124
CB274124.1 GI:28464447
EST.
Mus musculus (house mouse)
4 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Blomedical Research, Dept. of Genetics) - excision done by B.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, Ritter, E., Tsagareishvili, R., Ronko, I., Maguire, L., Bennett, J., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 50)
McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
Marrin T. Wvlie.T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:2072492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: McCarrey/Eddy NIEHS Mouse
                    Similarity
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h quality sequence stop: 52.
Location/Qualifiers
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314 286 1810
                                                                                  /tissue type="round spermatids, pooled from multiple mice"
/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/clone_lib="McCarrey Eddy round spermatid"
/note="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site 1: XhoII; Site 2: EcoRI; CDNA oligo
dT-primed [5'-(GA)I0-ACTAGTCTCGAGTTTTTTTTTTTTTTTTT']') and
directionally cloned using 5' linkers 5'-AATTCGGCACGAG-3'
and 5'-CTCGTGCCG-3'. Size selection of *400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UniZAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98.5% recombinants.

References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63423."
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55.0%; Score 11; DB 6; Lilarity 100.0%; Pred. No. 5.9e+04; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="CD-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:6448532"
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AF219060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r
http://baygenomics.ucsf.edu/
Unpublished (2001)
On Apr 1, 2004 this sequence version replaced gi:30109402.
On Apr 1, 2004 this sequence version replaced gi:30109402.
Contact: BayGenomics
Day Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
                                                                                                                                                                                                                                                                                                                                                                                                     CC156046 60
NPX123 BayGenomics Gene Trap
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University of Nottingham
Queen's Medical Center, Nottingham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Hamshere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Mammalia; Eutheria;
1 (bases 1 to 60)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="G£9"
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Rodentia;
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Library pGT1δTMpfs Mus musculus
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GSS 01-APR-2004

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Gaps

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CB264514
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                                                                                                                   DEFINITION
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CR042871/c
LOCUS
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                                                                                 CB264514
54-E020827-035-004-P01g-T7R MPIZ-ADIS-035 Arabidopsis thaliana cDNA clone MPIZP2000P014Q 5-PRIME, mRNA sequence.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                        Arabidopsis thaliana (thale cress)
                                                                CB264514.1 GI:32889287
                                                                                                                                                                                                                        5 TGCCACTCCCA 15
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 60)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GR042871 60 bp DNA linear GSS 05-JUL-200 Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP272c17, genomic survey sequence.
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                                                                                                                                                                                             TGCCACTCCCA 20
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OPTION=EXACT&TYPE=CELL_LINE&KEY=NPX123
Class: Gene Trap.
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                                                                                                                                                                                                                                                 55.0%; Score 11; DB 9; Lilarity 100.0%; Pred. No. 5.9e+04; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP2"72c17"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/mol_type="mRNA"
/strain="129 ola"
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Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus 1 (bases 1 to 65)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weise,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 CTCCCATTCTT 20
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10038008R Mouse 10kb plasmid UUGC1M library Mus mclone UUGC1M0338008 R, genomic survey sequence.
                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                AZ500380.1 GI:10680138
                                                                                                                                                                                                                                       Mus musculus (house mouse)
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Insert Length: 64 Std Error: 0.00
Plate: 4 row: P column: 01
Seq primer: T7R; CTAATACGACTCACTATAGGGA.
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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Large-scale identification and analysis of genome-wide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="MPIZ-ADIS-15"
/clone_lib="MPIZ-ADIS-25"
/note="Vector: psport1; Site 1: SalI; Site 2: Not1; cDNA
library from Arabidopsis thaliana, accession Achkarren-2;
inflorescences from flower buds to young siliques; library
was made at the Max-Planck-Institute for Plant Breeding
Primer sites and orientation;
T7-SalI-CCACGCGTCG-5prime-cDNA-POLYA-CC-NotI-SP6; Note:
Sequencing granted in the context of the GABI Arabidopsis
Sequencing granted in the context of the GABI Arabidopsis
high-efficiency SNP-based mapping tools and development of
methods for genome-wide mutation detection' PI: Bernd
Weisshaar; Sequence submission managed by
is available from RZPD; contact RZPD (clone@rzpd.de ) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/mol_type="maNNA"
/cultivar="Achkarren-2 (Ak-2)"
/db_xref="GABI:594855"
/db_xref="taxon:3702"
/clone="MPIZp2000P014Q"
/tissue_type="inflorescence"
/lab_host="E._coli_TOP10"
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100.0%; Pred. No. 5.9
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        musculus genomic
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TITLE
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Insert Length: 10000 Std Error: (
Plate: 0338 row: O column: 08
Seg primer: CACACAGGAAACAGCTATGACC
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 66) Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                          chromosome engineering clone MHPP115n17, genomic CR038728 CR038728.1 GI:49771783
                                                                                                                                                                                                                                                                                                                     CR038728 66 bp DNA linear GSS 05-JUL-20 Forward strand read from insert in 3'HPRT insertion targeting and
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                                                                                                                                                                                                                      GSS; genome survey sequence; MICER.
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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100.0%; Pred. No. 5.9e+04;
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                                                                                                                                                                                                                                                                                                survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Nouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ465119 68 bp DNA linear GSS 0.
1M0274A22R Mouse 10kb plasmid UUGCIM library Mus musculus
clone UUGC1M0274A22 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: A column: 22
Seg_primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B.
University of Utah
University of Utah
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Location/Qualifiers
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /Clone lib="Mouse 10kb plasmid UUCCIM library" /note="Vector: pW042nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S.
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/db_xref="taxon:10090"
/clone="MHPP115n17"
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                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0274A22"
                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                             /sex="Male"
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100.0%; Pred. No. 5.9e+04;
tive 0; Mismatches 0;
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RESULT 41
CN927075
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CL888998
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Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methylation filtered genomic sequences Unpublished (2004)
Contact: Gary Stacey
University of Missouri
108 Maters Hall, Columbia, MO 65211, US
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 573-884-1267
Fax: 573-882-0588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D. Peterson,S., Jones,J., Fries,J., Budiman,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (soybean)
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CL888998 69 bp DNA abf93b07.x1 Soybean random, unfiltered genomic, genomic survey sequence. CL888998 CL888998.1 GI:51632383 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: staceyg@missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CCACTCCCATT 17
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                                                                                                                                                                                                                           /tissue_type="Young leaves" /tissue_type="Young leaves" /clone_lib="Soybean random, unfiltered genomic library" /note="Vector: pOT2, Site 1: BstXI, Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                          /organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
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Matches 11
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                                                                                       Stanford University
855 California Ave, F
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
Email: walbot@stanford.edu
Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1006147 row: 8
Class: transposon-tagged.
                                                                                                                                                                           Maize genomic sequences Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 72)
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BH228652
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1006147H09.2EL_x1 1006 -
                                                                                                                                                         Department of Biological Sciences
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Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
MCArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,B. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Facility
The Horticulture an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malus x domestica (cultivated apple) Malus x domestica
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72 bp mRNA
000529AEPA002800HT (AEPA) Pinkie expanding
cDNA clone AEPA002800, mRNA sequence.
CN927075
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Conservative (
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Location/Qualifiers
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/clone lib="(AEPA) Pinkie expanding leaf"
/note="Vector: pBK-CMV; Library sequenced
Research & Development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="ABPA002800"
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ive 0; Mismatches
                                                                                                                         Palo Alto,
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                                                                                                                                                                                                                                                                                                                                                                                                               RescueMu
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                                                                                                                       94304,
                                 by 2 different endonucleases. sequence from source sequence.
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RESULT 44
BG866118
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CR055514
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Best Local
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Best Local Similarity
Matches 11; Conserv
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                                                                                             42
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                                                                                                                              μ
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-FEB-2004) Sanger Centre, Hinxt CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, D.J., Biggs, P.J., Cox, A.V., Jonkers, J., Smith, J., Plumb, R.W., Rogers, J. and Bradley, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 72)
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CR055514.1 GI:49788653
GSS; genome survey sequence; MICER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR055514 72 bp DNA linear GSS 05-JUL-200 Forward strand read from insert in 3'HRT insertion targeting and chromosome engineering clone MHPP136i08, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                             GCATTGCCACT 52
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                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="1006 - RescueMu Grid G"
/clone lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu; Site_2: BglII;
pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified malze Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
unites. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ampicillin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP136108"
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100.0%; Pred. No. 6e-
cive 0; Mismatches
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Pred. No.
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6e+04;
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6e+04;
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Taylor,R.G.,
   mRNA
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Nishijima,I., Yu,Y
   EST 29-MAY-2001
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                                                                                                                         TITLE
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
plate: LLAM10812 row: f column: 12

High quality sequence stop: 73.

Location/Qualifiers
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pederse Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., vo Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                       AZ430790 74 b
1M0215K19F Mouse 10kb plasmid
clone UUGC1M0215K19 F, genomic
AZ430790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                         Mouse whole genome scaffolding
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10090" /cloine="IMAGE:4910987" /cloine="IMAGE:4910987" /lab host:"DH10B (TI phage-resistant)" /cloine_lib="NCI_CGAP_SG2" /cloine_lib="NCI_CGAP_SG2" /cloine_lib="NCI_CGAP_SG2" /cloined_lib="NCI_CGAP_SG2" /cloined_lib="CMV-SPORT6; Site_1: NotI; Site_2: Salivary gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1: NotI; CGAP_Library."
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Rodentia;
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Pred. No. 6e+04;
Mismatches 0
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                                                                                                                         with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                            survey sequence.
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      E)
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Search completed: September 14, 2005, 11:43:51 Job time : 2421 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0215 row: K column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 74.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@gene
                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from M.
musculus_C57EL/6J (male) was obtained from the Jackson
Laboratory Mouse_DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWm92 (gil4732114/gb)AF122072.1), a copy-number
inducible_derivative_of_plasmid_R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse_DNA was annealed to
adaptored vector_DNA, and transformed_into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
/db xref="taxon:10090"
/clone="UUGCIM0215K19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Male"
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Minimum DB
Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     Score
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 Issued_Patents_NA: *
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Copyright (c) 1993 - 2005 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                    Length
  BB
US-08-956-171E-2606
US-08-781-966A-2606
US-09-262-773-113
US-09-396-196G-16433
US-09-396-196G-106333
US-09-396-196G-106333
US-09-396-196G-106333
US-09-396-196G-106333
US-09-396-196G-106333
US-09-08-100-297-8
US-09-08-100-297-8
US-09-09-180A-5
US-09-990-180A-5
US-09-990-180A-5
US-09-396-196G-26004
US-09-396-196G-26005
US-09-396-196G-26005
US-09-396-196G-72679
US-09-396-196G-72679
US-09-396-196G-72679
US-09-396-196G-72679
US-09-396-196G-72679
US-09-396-196G-72679
US-09-396-196G-72679
US-09-396-196G-72680
US-08-645-641-3
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US-08-800-353-408B-32
US-08-800-353-408B-32
US-08-800-353-24
US-08-800-353-24
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268.242 Million cell updates/sec
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Sequence 12606, Ap
Sequence 113, App
Sequence 64405, A
Sequence 106332,
Sequence 106333,
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Sequence
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US-08-956-171E-2606/c
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ALIGNMENTS	US-10-141-060-15	US-10-141-094-15	US-10-141-063-15	US-10-141-103-15	US-10-141-021-15	US-09-696-791-3882	US-09-696-791-3881	US-09-422-978-5302	US-09-155-885A-267	US-09-422-978-8213	US-09-213-719-54	US-09-081-646-830	US-09-081-646-147	US-08-441-887A-59	PCT-US92-10983-32	PCT-US92-06185-24	US-08-758-417A-48	US-09-042-353-200	
	Sequence 1	Sequence 3	Sequence 3	Sequence 5		Sequence 8				Sequence 5	Sequence 3	Sequence 2	Sequence 48,	Sequence 2					
	5, Appı	5, Appi	15, Appi	15, Appl	•	3882, Ap	881, Ap	302, Ap	267, App	8213, Ap	54, Appi	830, App	47, App	59, App1	2, Appl	4, Appi	Hddy '8	_	

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US-08-956-171E-2606
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2606:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4M

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION NUMBER: US/08/956,171E

PILING DATE: 20-Oct-1997

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY AGENT INFORMATION:

NUMBER: MSTATE JANUARY

ATTORNEY MSTATE JANUARY

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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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STREET: 9410 Key West
CITY: Rockville
STATE: Maryland
                                                                                                                                             STRANDEDNESS: double
                                                                                                                                                                                           LENGTH: 54 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                  DESCRIPTION: SEQ ID NO: 2606:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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West Avenue
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Length 54

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    GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Hegner, Susanne
APPLICANT: Hegs, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-781-986A-2606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2606: SEQUENCE CHARACTERISTICS: LENGTH: 54 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                    Sequence 113, Application US/09262773 Patent No. 6225451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.0%; Score 13; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e+6 Matches 13; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/262,773
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Best Local Similarity 100.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKST NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Diskett
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STREET: 9410 Key West Avenue
CITY: Rockville
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Y: USA
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5255
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Sequence 106332, Application US/09396196G
Patent NO. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTMARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 644405

LENGTH: 25

Type: nna
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106332
                                                                                                                                                                                                                                                                                                                                                                       US-09-396-196G-106332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-64405
                                                                         PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 21
; TYPE: DNA
; ORGANISM: primer
US-09-262-773-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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NUMBER OF SEQ ID NOS: 210
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 113
LENGTH: 21
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Best Local Similarity
Matches 12; Conserva
                                                           ENGTH: 25
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o. 6821724
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Pred. No. 6.1e+02;
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Query Match Best Local

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Gaps

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60.0%;

Score 12; Pred. No. Mismatches

DB 4; 6.1e+02;

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GCATTGCCACTC 18

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В
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                                                                                                                                      ; ORGANISM: mus musculus
US-09-396-196G-106334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: mus musculus
US-09-396-196G-106333
                                                                  Query Match
Best Local S
Matches 12
                                                                                                                                                                 NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 106334
LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106333
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 199-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                         APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Michael Mittmann APPLICANT: David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                  Similarity
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 GCATTGCCACTC 14
                                   GCATTGCCACTC 12
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                                                                    Conservative
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                                                                  60.0%; Score 12; DB 4; L
100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0;
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US-08-846-012A-8/c
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TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08846012A
Patent No. 5807740
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Patent No. 5849514
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                APPLICANT: AMARAL, M. Cathe APPLICANT: CHEN, Jin-Long TITLE OF INVENTION: Regulat NUMBER OF SEQUENCES: 16 CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UNMER: 36,627
REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: AMARAL, M. Cat
APPLICANT: CHEN, Jin-Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FITLE OF INVENTION: Regulators of UCP2 Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/846,012A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                ZIP: 94104
                                                                                                                                                                   STATE:
                                                                                                                                                                                                    STREET:
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                               SSEE: SCIENCE & TECHNOLOGY LAW GROUP
T: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
: CALIFORNIA
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US/09/100,297
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; Pred. No. 6.1e+0
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NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018781-000600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-052-995-8/c
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION WUMBER: US/09/052,995
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patent Assortes
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-
TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sivaraj
APPLICANT: Strulov
APPLICANT: Flores,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09052995
Patent No. 6183956
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TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Flores, Osvaldo A.
TITLE OF INVENTION: High Throughput In Vitro Screening Assay
TITLE OF INVENTION: for Transcription Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0:
                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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                            FH: 39 base pairs : nucleic acid NDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 TTGCCACTCCCA 9
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12; Conserv
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100.0%; Pred. No.
tive 0; Mismatc
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6.le+02;
hes 0; Indels
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COUNTRY: US.A.

ZIP: 90071-2066

ZONDUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION UNBER: TILING DATE:
APPLICATION UNBER: TILING DATE:
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
RESULT 12
US-09-690-185A-5/c
; Sequence 5, Application US/09690185A
; Patent No. 6471964
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                                                                                                                                                                                                                                               US-08-758-306-997
                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                   Query Match 55.0%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-758-306-997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stinchcomb
APPLICANT: McSwiggen,
TITLE OF INVENTION: M
TITLE OF INVENTION: M
TITLE OF INVENTION: A
TITLE OF INVENTION: A
TITLE OF INVENTION: G
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Culfornia
COlumny. Culfornia
                                                                                                                                  2 CATTGCCACTC 12
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                                                                                                       CAUUGCCACUC
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5807743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASSOCIATED WITH
INTERLEUKIN-2 R
                                                                                                                                                                  Score 11; DB 1;
Pred. No. 2.3e+03;
3; Mismatches 0
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                                                                                                                                                                                                 Length 17,
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GENERAL INFORMATION:

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                                                                                                                                                             RESULT 14
US-09-230-196-46
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Best Local S
Matches 11
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                                                                                                                     Sequence 46, Application US/09230196 Patent No. 6307035
                                                                                                                                                                                                                                                                                                                        Matches . 11; Conservative
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CURRENT APPLICATION NUMBER: US/09/690,185A
CURRENT FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: EP99203401.7
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 8
GENERAL INFORMATION:
APPLICANT: Rauscher III, Frank J.
APPLICANT: Jensen, David E.
TITLE OF INVENTION: BRCA1 Associa
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/853,164C CURRENT FILING DATE: 1997-05-08 PRIOR APPLICATION NUMBER: 60/016,590 PRIOR FILING DATE: 1996-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Roy , Arun K.
APPLICANT: Chen, SHEDIATED INACTIVATION OF THE ANDROGEN RECEPTOR TITLE OF INVENTION: RIBOZYME MEDIATED INACTIVATION OF THE ANDROGEN RECEPTOR FILE REFERENCE: 4003.001500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BIBRING, BIRIK
APPLICANT: KROSSOY, BJORN
TITLE OF INVENTION: DA ENCODING STRUCTURAL PROTEIN-1 OF INFECTIOUS SALMON
TITLE OF INVENTION: ANAEMIA VIRUS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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LOCATION: ()..()
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE FEATURE:
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ilarity 100.0%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 0;
באכאו Associated Protein
Uses Therefor
47
                                                                                                                                                                                                                                                                                                                                             55.0%; Score 11; DB 4; 1 100.0%; Pred. No. 2.3e+03
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; MOLECULE TYPE:
US-09-230-196-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09403861A
Patent NO. 6833348
GENERAL INFORMATION:
APPLICANT: RICCARDI, Carlo
TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: WS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,997
FILING DATE: 02-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,109
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19477
COMPUTER READABLE FORM:
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NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bak, Mary E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARB: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/403,861A
FILING DATE: 11-Feb-2000
PRIOR APPLICATION DATA:
                                                                                                                                          ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIWARK, P.L.L.C.
STREET: 624 Ninth Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                  COUNTRY: USA
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NUMBER: PCT/EP98/02490
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US-09-396-196G-26005
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     Sequence 26005, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
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US-09-396-196G-26004
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LOCATION: 1..20

OTHER INFORMATION: /note= "PCR reverse primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-403-861A-4
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17 NUMBER OF SEQ ID NOS: 127806 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 26004 LENGTH: 25
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26004, Application | Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: Bingle
TYPE: ODNA
HYPOTHETICAL: NO
FEATURE: CDNA
FEATURE: CDNA
                                                                                                                                                                                                                                     Local
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APPLICATION NUMBER: EP 97107033.9
FILING DATE: 28-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                               1 GCATTGCCACT 11
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David Mack
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David Lockhart
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REFERENCE/DOCKET NUMBER: RI
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llarity 100.0%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.3e+0
tive 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/396,196G; CURRENT FILING DATE: 1999-09-15; PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17; NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 26005
LENGTH: 25
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-26005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72679
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US-09-396-196G-72680
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-72679
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US-09-396-196G-72679
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Patent No. 6821724
GENERAL INFORMATION:
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APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6821724
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                   13 GCÁTTGCCÁCT 23
                                                                                                                                                                                                                                                                                                                                                                                                 1 GCATTGCCACT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
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                                                                                                                                                                                                                                                           Application US/09396196G
                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 11; DB 4; L
100.0%; Pred. No. 2.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%; Score 11; DB 4; L
100.0%; Pred. No. 2.3e+03;
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-72680
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; ORGANISM: mus musculus
US-09-396-196G-91273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 91273
                                                                                                                                                                                                                        Sequence 24, Application US/07834539A

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 72680
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Michael Mittmann APPLICANT: David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 1992-02-05
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David Lockhart
                                                                                                                                                                      USA
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100.0%; Pred. No. 2.3e+03;
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                 US/07/834,539A
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 Mismatches

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US-08-053-131-32/c
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COMPUTER: IBM PC Compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PAtentin Release #1.0, Version #1.25
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/88/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
PILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TO 07/857 ANR
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Best Local Similarity
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TELEPANE: 415-543-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                        APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 42 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One runcisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Trans
TITLE OF INVENTION: Produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                   SEQUENCE CHARACTERISTICS
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LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic No. 5661016-Human Animals for Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%; Score 11;
100.0%; Pred. No.
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                                                                                                                                                                            14643-9-3
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US-07-853-408B-32/c
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FILING DATE: 23-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REPERENCE/DOCKET NUMBER: 14643-000913

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2440

TELEPAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
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US-08-645-641-32/c
; Sequence 32, Appl:
; Patent No. 571903;
                                                                                                                                                                                                         Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                            US-08-645-641-32
                                               Sequence 32,
Patent No. 5
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GENERAL INFORMATION:
APPLICANT: Lonber:
APPLICANT: Kay, Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPACIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, VE

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/645,641

FILING DATE: 20-MAY-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

ADDITION APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: Lonber
APPLICANT: Kay, R
                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (primer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                             11 CACTCCCATTC 1
                                                                                                                                                                                                           l Similarity
11; Conserv
                                                                                                                                                                        8 CACTCCCATTC 18
                                             2, Application US/07853408B 5789650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (primer)
                                                                                                                                                                                                                  55.0%; Score 11; DB 1; I 100.0%; Pred. No. 2.4e+03;
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100.0%; Pr
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2.4e+03;
hes 0; Indels
                                                                                                                                                                                                                                  Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1464
TELECOMMUNICATION INFORMATION:
TELEPIONE: 415-326-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5814318
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/08096762
Patent No. 5814318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
                                                     APPLICATION NUMBER: US/08/096,762 FILING DATE: 22-JUL-1993 CLASSIFICATION: 800
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Transgenic No. 5789650-Human Anim
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                         COUNTRY: U
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                          California
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                                                                                                                      Version #1.25
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2.4e+03;
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-DEC-

IMBER: US 07/990,860

APPLICATION NUMBER: FILING DATE: 23-JUN

23-JUN-1992

US 07/904,068

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RESULT 26
US-08-800-353-24/c
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Best Local Similarity
Matches 11; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/834
PILING DATE: 1992-02-05
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1464
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucreate strandedness: since topology: linear topology: DNA
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APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic
TITLE OF INVENTION: Producing
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                                                                                                                                                                                                                                                     MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                         APPLICATION NUMBER: US/08/800,353
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                                                                                                                                US/07/834,539
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; MOLECULE TYPE:
US-08-800-353-24
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                                                                                      ; TOPOLOGY: 1i; MOLECULE TYPE: US-08-308-865-32
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Patent No. 5877397
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Best Local S
                               Matches
                                             Query Match
Best Local Similarity
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                                                                                                                                                                                             TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
**CAPPLICATION NUMBER: US/08/308,865
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APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                     FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Transgenic No. 5877397-Human Animals TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lonberg, Nils APPLICANT: Kay, Robert M.
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                 LENGTH:
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   8 CACTCCCATTC 18
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                                                                                                        DNA (primer)
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                                           55.0%; Score 11; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                  US 07/904,068
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                                Mismatches
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2.4e+03;
                                              DB 2; L
2.4e+03;
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RESULT 28
US-09-042-353-200/c
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-UU-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
PRIOR APPLICATION NUMBER: US 08/155,301
PRIOR APPLICATION NUMBER: US 08/155,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
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                                                                                                                                                                           FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
                                                 PRIOR APPLICATION DATA:
                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
WO PCT/US96/16433
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                                                                                                                              FILING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/728,463
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US 08/758,417 FILING DATE: 02-DEC-1996
                                                                                                                          APPLICATION NUMBER: US 01 FILING DATE: 10-OCT-1996
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0
FILING DATE: 23-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48, Application US/08758417A
PATENT NO. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE 01-LL FILING DATE: 01-LL ATTORNEY/AGENT INFORMATION:
ATTORNEY APPLE, RANDOLPH T.
APPLE, NUMBER: 36,429
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION DATE: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 55.0%; Sc. Local Similarity 100.0%; Portion 0;
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILLING DATE: 02-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 CACTCCCATTC 1
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                      APPLICATION NUMBER: US 08/096,762 FILING DATE: 22-JUL-1993
                                                             APPLICATION NUMBER: US 08/155,301 FILING DATE: 18-NOV-1993
                                                                                              APPLICATION NUMBER: US 08/161,739 FILING DATE: 03-DEC-1993
                                                                                                                                    APPLICATION NUMBER: US 08/165,699 FILING DATE: 10-DEC-1993
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
ION NUMBER: US 08/053,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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Pred. No. 2.4e+03
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application PC/TUS9206185

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                       Matches
                                                         Query Match
Best Local (
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                                                                                                                                                                                    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
REFERENCE/DOCKET NUMBER: 1464
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS: ADDRESSE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PFILING DATE: 19910828 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94105
                                                         Local Similarity
                                                                                                                                                                       STRANDEDNESS:
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REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 48:
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                                       11; Conservative
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: California
   CACTCCCATTC 18
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                   single
                                                                                                                                 DNA (genomic)
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100.0%; Pred. No. 2.4e+03;
tive 0; Mismatches 0;
                                                         55.0%; Score 11; DB 5; I 100.0%; Pred. No. 2.4e+03;
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                                       Mismatches
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                                                                                                                                                                                                                                        Patent No. 5837832
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          Sequence 59
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SMICH, WILLIAM M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 1i MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                  APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: Biological Chips
                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                        APPLICANT:
                                                                                                     APPLICANT:
                                                                                                                    APPLICANT:
                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application PC/TUS9210983
                                                                                                                                                                                                                                                                          Application US/08441887A
                                                                                                                                Cronin, Maureen T.
Fodor, Stephen P.A.
Huang, Xiaohua X.
Hubbell, Earl A.
Lipshutz, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                    Lobban, Peter E.
Morris, Macdonald S.
                                                                                                                                                                                                                        Chee, Mark
Townsend and Townsend and Crew LLP
                   ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (primer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%; Score 11; 100.0%; Pred. No.
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F: Two Embarcadero Center, 8th Floor San Francisco : California

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
FILING DATE: 16-MAY-1995
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION DATA
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993

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Sequence 54, Application US/09213719B
Patent No. 6150162
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION
CURRENT APPLICATION NUMBER: US/09/213,719B
CURRENT APPLICATION NUMBER: US/09/213,719B
NUMBER OF SEQ ID NOS: 91
LENGTH: 18
TYDE: DNA
OBGANISM: Artificial Sequence
FEATURE:
OPTIER INFORMATION: Antisense Oligonucleotide
US-09-213-719-54
RESULT 36
US-09-422-978-8213/c
; Sequence 8213, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
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Best Local S
Matches 10
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US-09-213-719-54
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APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
TITLE OF INVENTION: Gene Expression Profiles in
TITLE OF INVENTION: Cancer Cells
FILE REFERENCE: 01107.74664
CURRENT APPLICATION NUMBER: US/09/081,646
EARLIER APPLICATION NUMBER: 60/047,352
BARLIER FILING DATE: 1997-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 871
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 830
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100 les 10; Conservative
                                                                                                                                                                                         10;
                                                                                                                                                     2 CATTGCCACT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ccacrcccar 2
                                                                                                                                                                                                    Similarity
                                                                                                                    CATTGCCACT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 CCACTCCCAT 16
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o. 6333152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 CCACTCCCAT 2
                                                                                                                                                                                  illarity 100.0%; Score 10; DB 3; L
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACTCCCAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 10; DB 3; Length 15; 100.0%; Pred. No. 8.9e+03; rative 0; Mismatches 0; Indels
                                                                                                                                                                             Mismatches
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US-08-441-887A-59

TOPOLOGY: 11

DNA (probe)

LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:

CLASSIFICATION: 435
PRIOR APPLICATION DATA,
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:

Query Match 50.0%; Score 10; DB 2; 1 Best Local Similarity 100.0%; Pred. No. 8.9e+03 Matches 10; Conservative 0; Mismatches 0.

Length 12; Indels

0,

Gaps

0

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CURRENT APPLICATION NUMBER: US/09/081,646
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: 60/047,352
EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 871
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 147
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-09-081-646-147
       Query Match
50.0%; Score 10; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-081-646-147/c
                                                                                                                                                                                                                                                                                                                                                  Sequence 147, Application US/09081646
Patent No. 6333152
GENERAL INFORMATION:
APPLICANT: Kinzler, Kenneth
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
FILE REFERENCE: 01107,74664
FILE REFERENCE: 01107,74664
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; NAME/KEY: primer bind
; LOCATION: 1..18 -
; OTHER INFORMATION: downstream amplification primer 99-14446
US-09-422-978-8213
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APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenkov, Ilya
TITLE OF INVENTION: Biallelic markers for use in
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-155-885A-267/c
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GENERAL INFORMATION:
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LENGTH: 18
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ORGANISM: Homo Sapiens
                     INFORMATION
                                                                      APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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les 10; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STUYVER, LIEVEN ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
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                   TELEPHONE: (703)
TELEFAX: (703) 8:
NN FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
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  CHARACTERISTICS
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                                         816-4100
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hes 0;
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RESULT 38
US-09-422-978-5302
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; FEATURE;
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-23334 for SEQ 1368, US-09-422-978-5302
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                                                                                                                                                                                                                                                                                               RESULT 39
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SEQ ID NO 5302
LENGTH: 19
TYPE: DNA
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FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3881
LENGTH: 19
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Best Local
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APPLICANT: Cohen, Daniel
APPLICANT: Elumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
                                                                                                                   TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: SKIN AND EYE DISEASES FILE REFERENCE: 480124.407
                                                                                                                                                                          APPLICANT: Robbins, Joan M. APPLICANT: Tritz, Richard
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECILE TYPE: DNA (genomic)
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100.0%; Pr
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100.0%; Pred. No.
tive 0; Mismatch
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Pred. No.
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8.9e+03;
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                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-10-141-021-15
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US-10-141-021-15/c
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US-09-696-791-3882
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APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 4"
FILE REFERENCE: 30034-93461
CURRENT FILLING DATE: 2002-05-08
RUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
LENGTH: 20
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                                                                       Query Match
Best Local (
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                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROBBINS, JOAN M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EYE DISEASES
FILE REFERENCE: 480124, 407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3882
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/10141021 Patent No. PP14777
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Best Local :
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Best Local S
                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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Local Similarity 100.0%; P
Les 10; Conservative 0;
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Local Similarity 100.0%; F
 11
                                                                      Similarity
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 ATTGCCACTC
                         ATTGCCACTC 12
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                                                       Conservative
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                                                                    50.0%; Score 10; 100.0%; Pred. No.
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Pred. No.
                                                      Mismatches
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                                                                    DB 1;
9e+03;
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9e+03;
hes 0; Indels
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9e+03;
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RESULT 44
US-10-141-094-15/c
| Sequence 15, Application US/10141094
| Patent No. PP14978
| GENERAL IMPORMATION:
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US-10-141-063-15/c
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APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED
FILE REFERENCE: 30034-93463
CURRENT APPLICATION NUMBER: US/10/141,094
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
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US-10-141-103-15/c
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SEQ ID NO 15
LENGTH: 20
TYPE: DNA
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SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                     Best Local
Matches 1
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PATENT NO. PP14829
GENERAL INFORMATION:
APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE FILE REFERENCE: 30034-93462
CURRENT APPLICATION UNMEER: US/10/141,103
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEC ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 10"
FILE REFERENCE: 30034-93467
CURRENT APPLICATION NUMBER: US/10/141,063
CURRENT FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 18
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Best Local (
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100.0%; Pred. No. 9e-
tive 0; Mismatches
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Pred. No.
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9e+03;
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9e+03;
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Sequence 15, Application US/10141060

Sequence 15, Application US/10141060

Patent No. Pp15079

GENERAL INFORMATION:
APPLICANT: BEINEKE, WALTER F.

TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 1"

FILE REFERENCE: 30034-92642

CURRENT APPLICATION NUMBER: US/10/141,060

CURRENT FILING DATE: 2002-07-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 20
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
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Search completed: September 14, 2005, 11:45:54 Job time : 124 secs
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73, A 19 12 60.0 20 19 US-10-303-635-74 Sequence 73, A 19 12 60.0 20 19 US-10-303-635-74 Sequence 73, A 19 12 60.0 20 19 US-10-303-635-74 Sequence 73, A 19 12 60.0 22 US-10-257-158A-5395 Sequence 73, A 19 12 60.0 25 21 US-10-719-900-198562 Sequence 73, A 19 12 60.0 25 21 US-10-719-900-198562 Sequence 26471 27 12 60.0 25 21 US-10-719-900-903513 Sequence 26471 28 12 60.0 25 21 US-10-719-900-903513 Sequence 26471 29 12 60.0 25 21 US-10-719-900-974937 Sequence 903551 20 12 60.0 25 21 US-10-809-189-106332 Sequence 903552 20 12 60.0 25 21 US-10-809-189-106333 Sequence 644053 21 12 60.0 25 22 US-10-803-527-215523 Sequence 644053 23 12 60.0 25 22 US-10-843-527-21553 Sequence 10633 24 12 60.0 25 22 US-10-843-527-21593 Sequence 20511 25 20 US-10-843-527-21593 Sequence 20511 26 20 25 22 US-10-843-527-21593 Sequence 20511 27 60.0 25 22 US-10-843-527-21593 Sequence 20511 28 20 20 20 20 20 20 20 20 20 20 20 20 20

## ALIGNMENTS

RESULT 1 US-10-643-801-35

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                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 20
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LENGTH: 20
TYPB: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sanjay Bhanot
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: WOULDATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
FILE REFERENCE: RTS-0678US
FILE REFERENCE: RTS-0678US
FILE REPERENCE: RTS-0678U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                   20;
                                                                                                            1 GCATTGCCACTCCCATTCTT 20
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                   0; Mismatches
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Pred. No. 0.031;
      20
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RESULT 4
US-10-643-801-158/c
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US-10-643-801-36
                                         NUMBER OF SEQ ID NOS:
SEQ ID NO 158
LENGTH: 20
                                                                                                                                                                                                  Sequence 158, Application US/10643801 Publication No. US20050043524A1 GENERAL INFORMATION:
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
FILE REFERENCE: RTS-06/78US
CURRENT APPLICATION NUMBER: US/10/643,801
CURRENT FILING DATE: 2003-08-18
NUMBER OF SEQ ID NOS: 230
SEQ ID NO 36
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITTLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION CURRENT APPLICATION NUMBER: US/10/643,801
CURRENT FILING DATE: 2003-08-18
NUMBER OF SEQ ID NOS: 230
SEQ ID NO 157
LENGTH: CONTROL OF SEQ ID NOS: 230
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; Sequence 157, Applic.
; Publication No. US20
; GENERAL INFORMATION:
                                                        APPLICANT: Sanjay Bhanot
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
FILE REFERENCE: RTS-0678US
CURRENT APPLICATION NUMBER: US/10/643,801
CURRENT FILING DATE: 2003-08-18
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Best Local (
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Best Local Similarity 100.
Matches 20; Conservative
TYPE: DNA
ORGANISM: H. sapiens
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TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
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Local Similarity 100.0%; Pred. No. 31;
1es 15; Conservative 0; Mismatches 0; Indels
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o. US20050043524A1
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100.0%; Pred. No. 0.031;
ative 0; Mismatches
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APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 136702

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-10-719-900-136702
                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-10-719-900-136702/c

i Sequence 136702, Application US/10719900
i Publication No. US20050026164A1
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                                             Query Match
Best Local Similarity 100.0%, p
Marches 13; Conservative 0;
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; ORGANISM: Mus musculus
US-10-719-900-415646
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US-10-719-900-415646
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Best Local Similarity 100.0%; F
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528:1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 415646

LENGTH: 25
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Best Local Similarity 100.
Matches 15; Conservative
23 TGCCACTCCCATT 11
                  5 TGCCACTCCCATT 17
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                                                                           65.0%; Score 13; DB 21; 100.0%; Pred. No. 4.9e+0;
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                                                             Mismatches
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                                                                           4.9e+02;
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RESULT 7
US-10-719-900-840616
; Sequence 840616, Application US/10719900
; Publication No. US20050026164A1

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GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

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Sequence 86272

Sequence 86272, Application US/10843527

Publication No. US20050136395A1

GENERAL INFORMATION:
APPLICANT: Michael Mittmann

APPLICANT: Eric Schell

TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1

CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT FILING DATE: 2004-05-10

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR FILING DATE: 2003-05-08

NUMBER OF SEG ID NOS: 238196

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SETURGER OF SEG ID NOS: 238196
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; ORGANISM: SARS Virus
US-10-843-527-86272
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US-10-719-900-840616
                                                                                                                                                                                                                                                                                                                         US-10-843-527-151905
CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT FILING DATE: 2004-05-10

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 238196

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 151905
                                                                                                                                                                                                                                                   Sequence 151905, Application US/10843527 Publication No. US20050136395A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 13; Conservative (
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CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
                                                                                                                                                              APPLICANT: Michael Mittmann
APPLICANT: Eric Schell
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Pred. No. 4.9e+0
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Sequence 650147, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR APPLICATION SUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQUENCE: 50147
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US-10-719-956-650147
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                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3
COMPUTER: HP Vectra 486/
                                                                                                                                                                OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Charles Kunsch
NAME: Benson, Bob
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                  APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                                                                                                                                                                                                                    STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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100.0%; Pr
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          30,446
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Pred. No.
   PB248PP
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4.9e+02;
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 260
SEQUENCE CHARACTERISTICS:

2606:

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RESULT 12
US-10-329-624-2606/c
JS-quence 2606, Application US/10329624
Publication NO. US20040043037A1
GENERAL INFORMATION:
Charles Kunsch
                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 2606: US-10-329-624-2606
                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION IDATA:
APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997
APPLICATION NUMBER: 08/099,861

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: PB248P1D1

TELEPHONE: (240) 314-1224

TELEPAX: (301) 309-8439

SEQUENCE CHARACTERISTICS:
LENGTH: 54 base naive
                Query Match
Best Local S
Matches 13
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
                                                                                                                       LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
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          Conservative
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  65.0%; Score 13; DB 18;
100.0%; Pred. No. 4.8e+02;
cive 0; Mismatches 0;
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. 4.8e+02;
                                      Length 54;
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  Indels
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Gaps
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
TYPE: DNA
TYPE: DNA
                                                                         Query Match
Best Local S
Matches 12
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US-10-257-017B-267933
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                                                                                                                                                                                                                                       Sequence 267933, Application US/10257017B
Publication No. US20040241651A1

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
LENGTH: 12

LENGTH: 12

TYPE: NUMBER OF SEQ ID NOS: 382046
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US-09-908-975-18015
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US-09-908-975-18015
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                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICH
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
FILE REFERENCE: 36688-0005
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APPLICANT: WASSERMA
APPLICANT: MINTZ, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 13; Conserva
                                                                 Similarity 100, 12; Conservative
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CCACTCCCATTC 12
                             CCACTCCCATTC 18
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MINTZ, Liat
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                                                             60.0%; but
100.0%; Pr
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                                                                                     Score 12;
Pred. No.
                                                                   Mismatches
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                                                                                 DB 20;
2e+03;
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4.8e+02;
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                                                                 Indels
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                                                             Gaps
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US-10-303-635-74
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Sequence 74, Application US/10303635

Publication No. US20040102621A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
FILE REFERENCE: RTS-0418
CURRENT APPLICATION NUMBER: US/10/303,635

CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 73, Application US/10303635
Publication No. US20040102621A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 73
LENGTH: 20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 CURRENT FILING DATE: 2002-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/303,635
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: RTS-0418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF FORKHEAD BOX
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                     60.0%; Score 12; DB 19; Length 20; 100.0%; Pred. No. 2e+03;
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Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-257-158A-5395/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 257
SEQ ID NO 192
LENGTH: 20
TYPE: DNA
ORGANISM: H. Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-303-635-192/c
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JS-10-257-158A-5395
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SEQ ID NO 74
LENGTH: 20
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Best Local Similarity
Matches 12; Conserv
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Publication No. US20040102621A1
                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 5395
LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5395, Application US/10257158A Publication No. US20050142543A1
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                                                                                                                                           APPLICANT: Kliman, Richard
APPLICANT: Kliman, Richard
TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC P
TITLE OF INVENTION: SEQUENCE DIFFERENCES USING LIGASE DETECTION REACTION
FILE REFERENCE: 19603/2834
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: PCT/US01/10958
PRIOR APPLICATION NUMBER: PCT/US01/10958
PRIOR FILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2000-04-14
NUMBER: OF SEQ ID NOS: 9544
COPTRADER: DESCRIPTION OF SEQ ID NOS: 9544
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COPTRADER: DESCRIPTION OF SEQ ID NOS: 9544
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CURRENT APPLICATION NUMBER: US/10/303,635
CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF FORKHEAD
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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              OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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100.0%; Pred. No.
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15 GCATTGCCACTC 4

US-10-257-158A-762/c Sequence 762, Applic Publication No. US20 GENERAL INFORMATION:

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APPLICANT: Zirvi, Monib
APPLICANT: Gerry, Mornan P.
APPLICANT: Gerry, Norman P.
APPLICANT: Gerry, Norman P.
APPLICANT: Ravis, Reyna
APPLICANT: Kliman, Richard
TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC AC
TITLE OF INVENTION: SEQUENCE DIFFERENCES USING LIGASE DETECTION REACTION
CURRENT APPLICATION NUMBER: US/10/257,158A
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: PCT/US01/10958
PRIOR APPLICATION NUMBER: US 60/197,271
PRIOR FILING DATE: 2000-04-14
SOFTWARE: Patentin version 3.1
FENCTH: 24
                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTMARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 198562

TURN: CNA
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US-10-719-900-198562/c
; Sequence 198562, Application US/10719900
; Publication No. US20050026164A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence US-10-257-158A-762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
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ORGANISM: Artificial Sequence
FEATURE:
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0. US20050142543A1
                                                                                 60.0%; Score 12; 100.0%; Pred. No.
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Pred. No.
                                                          Mismatches
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                                                                           DB 21; Length 25; . 2e+03;
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FILE FILE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE FERFERICE: 3528.1
FURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 264711
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-264711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 305113, Application US/10719900
FULL FORMATION:
APPLICANT: Xue Mei Zhou
FILLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR PILING DATE: 2002-11-20
VNUMBER OF SEQ ID NOS: 982914
SOPTMARE: Microarray Probe Sequence Listing Generator V 1.1
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US-10-719-900-903551
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        Sequence 903551, Application US/10719900
publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFRENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
CURRENT FILING DATE: 2003-11-20
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US-10-719-900-305113
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LENGTH: 25
TYPE: DNA
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Best Local
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US-10-719-900-264711
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PRIOR APPLICATION NUMBER: 60/427,808
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Publication No. US/20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
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100.0%; Pred. No.
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; Pred. No.
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. 2e+03;
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GCATTGCCACTC 8

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Conservative

Query Match
Cocal Similarity

; TYPE: DNA ; ORGANISM: Mus musculus US-10-719-900-198562

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Matches

12;

Conservative

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Query Match Best Local Similarity

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GCATTGCCACTC 16

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US-10-719-900-964504/c
; Sequence 964504, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-10-719-900-903551
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US-10-719-900-974937
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US-10-719-900-964504
                                                                                                                               ; ORGANISM: Mus musculus US-10-719-900-974937
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NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 903551
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 974937, Application US/10719900 Publication No. US20050026164A1 GENERAL INFORMATION:
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LENGTH: 25
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                                                                                                                                                                                                            SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 974937
                                                   Query Match 60.0%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 2e-Matches 12; Conservative 0; Mismatches
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: MACCOARTRY Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                               APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                           ENGTH:
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Local Similarity 100.0%;
hes 12; Conservative (
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US-10-809-189-106332
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US-10-809-189-64405
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                                                                                                                                                 ; ORGANISM: mus musculus 
US-10-809-189-106332
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LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                       SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106332
LENGTH: 25
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                                                                       Matches
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Best Local Similarity
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PRIOR FILING DATE: 1999-09-15
PRIOR PELICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
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APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc
                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 127806
                                                                                                                                                                                       TYPE: DNA
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Local Similarity 100.0%;
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                                   1 GCATTGCCACTC 12
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GCATTGCCACTC 18
                                                                       Conservative
                                                                     60.0%; Score 12; DB 21; 100.0%; Pred. No. 2e+03; tive 0; Mismatches 0
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Pred. No. 2e+03;
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RESULT 29 US-10-809-189-106333

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PAPPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/10/809,189

CURRENT FILING DATE: 2004-03-25

PRIOR APPLICATION NUMBER: US/09/396,196

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16334

TYPE: TANA
                                                                                                    US-10-843-527-19523
                                                                                                                          RESULT 31
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Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/99/936,196
PRIOR APPLICATION NUMBER: US/100,678
PRIOR APPLICATION NUMBER: 05/100,678
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 106333
ILENCTH: 28
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; ORGANISM: mus musculus
US-10-809-189-106334
                                 Sequence 19523, Application US/10843527 Publication No. US20050136395A1 GENERAL INFORMATION:
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; ORGANISM: mus musculus
US-10-809-189-106333
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APPLICANT: Michael Mittmann APPLICANT: Eric Schell
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APPLICANT: David Mack
APPLICANT: David Lockhart
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CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: MICROARRAY Probe Sequence Listing
SEQ ID NO 216202
LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: Bric Schell
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1
CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR APPLICATION NUMBER: 60/469,545
I PRIOR FILING DATE: 2003-05-08
I NUMBER OF SEQ ID NOS: 238196
I SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
; ORGANISM: SARS Virus
US-10-843-527-216202
                                                                                                                                                                                                                                                                                          US-10-843-527-216202/c
Sequence 216202, Application US/10843527
Dublication No. US20050136395A1
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US-10-843-527-20511
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                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Eric Schell
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: SARS Virus US-10-843-527-19523
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Publication No. US20050136395A1
GENERAL INFORMATION:
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SEQ ID NO 19523
LENGTH: 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: SARS Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                  Probe Sequence Listing Generator V 1.1
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100.0%; Pr
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Pred. No.
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Pred. No.
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2e+03;
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US-10-843-527-217190/c
; Sequence 217190, Application US/10843527
; Publication No. US20050136395A1
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US-10-719-956-166560/c
US-10-719-956-166560, Application US/10719956
; Publication No. US20040146910A1
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US-10-719-956-143538/c
                                                                                                                                                                                                                                   ; ORGANISM: Rattus norvegicus 
US-10-719-956-143538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: SARS Virus
US-10-843-527-217190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 143538, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
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Matches
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 143538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 217190
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xue Mei Zhou
                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                               Local Similarity es 12; Conserv
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12; Conservation
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                                                                                                      TGCCACTCCCAT 11
                                                                                                                                   TGCCACTCCCAT 16
                                                                                                                                                                 60.0%; Score 12; DB ilarity 100.0%; Pred. No. 2e-Conservative 0; Mismatches
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Pred. No.
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                                                                                                                                                                                    DB 22; Length 25; 2e+03;
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TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-166560
                                                                                                                                                                                                                                                                                                                                  RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-329530
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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-329531
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 329530
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 165560
                                                                  CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 329531
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                                                                                                                                                                                                                                                                         Sequence 329531, Application US/10719956 Publication No. US20040146910A1
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Best Local 9
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILS REFERENCE: 3527.1
                                                                                                                                                                                                    APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
                                                     LENGTH: 25
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12; Conserv
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2e+03;
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RESULT 40
US-10-025-806-257
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US-10-719-956-693459
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US-10-719-956-693459
APPLICANT: Malyankar, Uriel
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Haihong
APPLICANT: Ellerman, Karen
APPLICANT: Wolenc, Adam
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-224 AB
CURRENT APPLICATION NUMBER: US/10/025,806
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                    APPLICANT:
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Publication No.
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 693459
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Best Local :
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Publication No. US20040146910A1
GENERAL INFORMATION:
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Best Local (
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                                                                                                  Vernet, Corine
Shenoy, Suresh
Gunther, Erik
Millet, Isabelle
Tchernev, Velizar
Anderson, David
Gusev, Vladimir
Malyankar, Uriel
Zhong, Halhong
Ellerman, Karen
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Edinger, Shlomit
Gerlach, Valerie
Sciore, Paul
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Peyman, John
MacDougall, John
                                                                                                                                                                                                                                                                                                 Stone, David
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Ballinger, Robert
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100.0%; Pr
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100.0%; Pred. No. 2e+03;
tive 0; Mismatches 0; Indels
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Pred. No.
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. 2e+03;
ches 0; Indels
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US-10-813-638-478/c

US-10-813-638-478/c

i Sequence 478, Application US/10813638

publication No. US20040235026A1

GENERAL INFORMATION:

APPLICANT: Shinkets, Richard A.

APPLICANT: Leach, Martin D.

TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND TILE OF INVENTION: USE THEREOF

FILE REFERENCE: 15966-599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/257,876
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2000-12-21
PRIOR PRIOR PRIOR NUMBER: 60/257,876
PRIOR PRIOR PRIOR DATE: 2000-012-21
PRIOR APPLICATION NUMBER: 60/260,718
PRIOR APPLICATION NUMBER: 60/284,591
PRIOR APPLICATION NUMBER: 60/284,591
PRIOR APPLICATION NUMBER: 60/284,591
PRIOR PRIOR DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 352
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 257
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                        CURRENT APPLICATION NUMBER: US/10/813,638
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: 60/163,783
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1468
SOFTWARE: CURAGEN PATENT FORMATTE Version 0.9
SEQ ID NO 478
LENGTH: 51
TYPE: DNA
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        LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
                                                ORGANISM: Homo sapiens FEATURE:
NAME/KEY: allele
  FEATURE:
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FILING DATE: 2001-04-23
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FILING DATE: 2001-03-14
APPLICATION NUMBER: 60/278,150
FILING DATE: 2001-03-23
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FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/276,464 FILING DATE: 2001-02-08
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FILING DATE: 2001-01-24
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FILING DATE: 2000-12-18
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RESULT 42
US-09-908-975-15069/c
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US-09-908-975-17268
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LENGTH: 60
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Publication No. US20030165843A1
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Best Local Similarity
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
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ORGANISM: Homo sapiens
-09-908-975-15069
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APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLICONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
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APPLICANT: WASSERM
APPLICANT: MINTZ,
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APPLICANT: WASSERMAN,
APPLICANT: MINTZ, Eli
                                                  CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR PILING DATE: 2000-07-28
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LOCATION: (0)...(0)
OTHER INFORMATION: Accession number cg44005525
                  SOFTWARE: PatentIn version 3.0
                                     NUMBER OF SEQ ID NOS:
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NO 17268
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MINTZ, Liat
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; Pred. No. 1.9e+03;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-17268
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                                                                                            , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003215 US-10-257-017B-14062
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                                                                                                                                                                                TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations FILE REPERENCE: E01/1193/WO CURRENT FILING DATE: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 14062 LENGTH: 13
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Matches
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SEQ ID NO 14061
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity 100.
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Best Local Similarity
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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APPLICANT: Christian Pie
APPLICANT: Kurt Berlin
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                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                     TYPE: DNA
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Kurt Berlin
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nilarity 100.0%;
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; Pred. No. 7.9e+03;
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Pred. No. 1.9e+03
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